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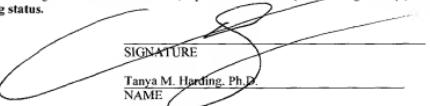
FORM PTO-1390 U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE		ATTORNEY'S DOCKET NUMBER
TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C. § 371		245-55928
INTERNATIONAL APPLICATION NO. PCT/US99/08744		U.S. APPLICATION NO. (If known, see 37 C.F.R. § 15) 09/673763
INTERNATIONAL FILING DATE 20 April 1999		PRIORITY DATE CLAIMED 20 April 1998
TITLE OF INVENTION CHLAMYDIA PROTEINS AND THEIR USES		
APPLICANT(S) FOR DO/EO/US Rockey and Bannantine		
<p>Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:</p> <ol style="list-style-type: none"> <input checked="" type="checkbox"/> This is a FIRST submission of items concerning a filing under 35 U.S.C. § 371. <input type="checkbox"/> This is a SECOND or SUBSEQUENT submission of items concerning a filing under 35 U.S.C. § 371 <input type="checkbox"/> This express request to begin national examination procedures (35 U.S.C. § 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. § 371(b) and PCT Articles 22 and 39(1) <input checked="" type="checkbox"/> A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date <input checked="" type="checkbox"/> A copy of the International Application as filed (35 U.S.C. § 371(c)(2)) <ol style="list-style-type: none"> <input checked="" type="checkbox"/> is transmitted herewith (required only if not transmitted by the International Bureau). <input type="checkbox"/> has been transmitted by the International Bureau. <input type="checkbox"/> is not required, as the application was filed in the United States Receiving Office (RO/US) <input type="checkbox"/> A translation of the International Application into English (35 U.S.C. § 371(c)(2)) <input checked="" type="checkbox"/> Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. § 371(c)(3)) <ol style="list-style-type: none"> <input type="checkbox"/> are transmitted herewith (required only if not transmitted by the International Bureau). <input type="checkbox"/> have been transmitted by the International Bureau <input type="checkbox"/> have not been made; however, the time limit for making such amendments has NOT expired. <input checked="" type="checkbox"/> have not been made and will not be made <input type="checkbox"/> A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. § 371(c)(3)). <input checked="" type="checkbox"/> An oath or declaration of the inventor(s) (35 U.S.C. § 371(c)(4)). <input type="checkbox"/> A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. § 371(c)(5)) 		
Items 11. to 16. below concern document(s) or information included:		
<ol style="list-style-type: none"> <input checked="" type="checkbox"/> An Information Disclosure Statement under 37 C.F.R. §§ 1.97 and 1.98, including copies of references cited in International Search Report. <input checked="" type="checkbox"/> An assignment document for recording. A separate cover sheet in compliance with 37 C.F.R. §§ 3.28 and 3.31 is included <input checked="" type="checkbox"/> A FIRST preliminary amendment. <input type="checkbox"/> A SECOND or SUBSEQUENT preliminary amendment <input type="checkbox"/> A substitute specification <input type="checkbox"/> A change of power of attorney and/or address letter. <input checked="" type="checkbox"/> Other items or information. <ul style="list-style-type: none"> <input type="checkbox"/> Written Opinion. <input type="checkbox"/> Preliminary Examination Report. <input checked="" type="checkbox"/> International Search Report <input type="checkbox"/> Computer Readable Form of Sequence Listing. <input type="checkbox"/> Statement in Compliance with 37 C.F.R. §1.821(f) 		



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532 Rec'd PCT/PTO 16 OCT 2000

U.S. APPLICATION NUMBER OR INTERNATIONAL FILING NUMBER (PCT/US99/08744)		INTERNATIONAL APPLICATION NO PCT/US99/08744	ATTORNEY'S DOCKET NUMBER 245-55928																																																		
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<p>17. <input checked="" type="checkbox"/> The following fees are submitted:</p> <p>BASIC NATIONAL FEE (37 C.F.R. §§ 1.492(a)(1)-(5):</p> <p>Neither International Preliminary Examination fee (37 C.F.R. § 1.482) nor International Search fee (37 C.F.R. § 1.445(a)(2)) paid to USPTO and International Search Report not prepared by the EPO or JPO..... \$1,000.00</p> <p>International Preliminary Examination fee (37 C.F.R. § 1.482) not paid to USPTO but International Search Report prepared by the EPO or JPO..... \$860.00</p> <p>International Preliminary Examination fee (37 C.F.R. § 1.482) not paid to USPTO but International Search fee (37 C.F.R. § 1.445(a)(2)) paid to USPTO..... \$710.00</p> <p>International Preliminary Examination fee paid to USPTO (37 C.F.R. § 1.482) but all claims did not satisfy provisions of PCT Article 33(1)-(4)..... \$690.00</p> <p>International Preliminary Examination fee paid to USPTO (37 C.F.R. § 1.482) and all claims satisfied provisions of PCT Article 33(1)-(4)..... \$100.00</p>																																																					
<p>ENTER APPROPRIATE BASIC FEE AMOUNT = \$ 690.00</p> <p>Surcharge of \$130.00 for furnishing the oath or declaration later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 C.F.R. § 1.492(e)).</p> <table border="1"> <thead> <tr> <th>CLAIMS</th> <th>NUMBER FILED</th> <th>NUMBER EXTRA</th> <th>RATE</th> </tr> </thead> <tbody> <tr> <td>Total claims</td> <td>18 - 20 =</td> <td>0</td> <td>x \$18.00 \$ 0.00</td> </tr> <tr> <td>Independent Claims</td> <td>7 - 3 =</td> <td>4</td> <td>x \$80.00 \$ 320.00</td> </tr> <tr> <td colspan="2">MULTIPLE DEPENDENT CLAIM(S) (if applicable)</td> <td></td> <td>+ \$270.00 \$</td> </tr> <tr> <td colspan="4">TOTAL OF ABOVE CALCULATIONS = \$ 1010.00</td> </tr> <tr> <td colspan="4">Reduction of 1/2 for filing by small entity, if applicable. A Small Entity Statement must also be filed. (Note 37 C.F.R. § 1.9, 1.27, 1.28)</td> </tr> <tr> <td colspan="4">SUBTOTAL = \$ 1010.00</td> </tr> <tr> <td colspan="4">Processing fee of \$130.00 for furnishing the English translation later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 Months from the earliest claimed priority date (37 C.F.R. § 1.492(f)).</td> </tr> <tr> <td colspan="4">TOTAL NATIONAL FEE = \$ 1010.00</td> </tr> <tr> <td colspan="4">Fee for recording the enclosed assignment (37 C.F.R. § 1.21(h)). The assignment must be Accompanied by an appropriate cover sheet (37 C.F.R. §§ 3.28, 3.31). \$40.00 per property. +</td> </tr> <tr> <td colspan="4">TOTAL FEES ENCLOSED = \$ 1050.00</td> </tr> <tr> <td colspan="4"> <table border="1"> <tr> <td>REFUND → \$</td> </tr> <tr> <td>CHARGE → \$</td> </tr> </table> </td> </tr> </tbody> </table>				CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE	Total claims	18 - 20 =	0	x \$18.00 \$ 0.00	Independent Claims	7 - 3 =	4	x \$80.00 \$ 320.00	MULTIPLE DEPENDENT CLAIM(S) (if applicable)			+ \$270.00 \$	TOTAL OF ABOVE CALCULATIONS = \$ 1010.00				Reduction of 1/2 for filing by small entity, if applicable. A Small Entity Statement must also be filed. (Note 37 C.F.R. § 1.9, 1.27, 1.28)				SUBTOTAL = \$ 1010.00				Processing fee of \$130.00 for furnishing the English translation later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 Months from the earliest claimed priority date (37 C.F.R. § 1.492(f)).				TOTAL NATIONAL FEE = \$ 1010.00				Fee for recording the enclosed assignment (37 C.F.R. § 1.21(h)). The assignment must be Accompanied by an appropriate cover sheet (37 C.F.R. §§ 3.28, 3.31). \$40.00 per property. +				TOTAL FEES ENCLOSED = \$ 1050.00				<table border="1"> <tr> <td>REFUND → \$</td> </tr> <tr> <td>CHARGE → \$</td> </tr> </table>				REFUND → \$	CHARGE → \$
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<p>a. <input checked="" type="checkbox"/> A check in the amount of \$ 1050.00 to cover the above fees is enclosed.</p> <p>b. <input type="checkbox"/> Please charge my Deposit Account No. _____ in the amount of \$ _____ to cover the above fees. A duplicate copy of this sheet is enclosed.</p> <p>c. <input checked="" type="checkbox"/> The Director is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. 02-4550. A duplicate copy of this sheet is enclosed</p>																																																					
<p>NOTE: Where an appropriate time limit under 37 C.F.R. § 1.494 or § 1.495 has not been met, a petition to revive (37 C.F.R. § 1.137(a) or (b)) must be filed and granted to restore the application to pending status.</p>																																																					
<p>SEND ALL CORRESPONDENCE TO:</p> <p>KLARQUIST SPARKMAN CAMPBELL, LEIGH & WHINSTON, LLP One World Trade Center, Suite 1600 121 S.W. Salmon Street Portland, OR 97204-2988</p>																																																					
<p>SIGNATURE  Tanya M. Harding, Ph.D. NAME _____</p> <p>42,630 REGISTRATION NUMBER _____</p>																																																					

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PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Rockey and Bannantine

Art Unit: Not yet assigned

Application No.: Not yet assigned

CERTIFICATE OF MAILING

Filed: Herewith

I hereby certify that this paper and the documents referred to as being attached or enclosed herewith are being deposited with the United States Postal Service on October 16, 2000 via Express Mail in an envelope addressed to: BOX PATENT APPLICATION, COMMISSIONER FOR PATENTS, WASHINGTON, D.C. 20231.

For: CHLAMYDIA PROTEINS AND THEIR USES

Examiner: Not yet assigned

Date: October 16, 2000


Tanya M. Harding, Ph.D.
Attorney for Applicant

BOX PATENT APPLICATION
COMMISSIONER FOR PATENTS
WASHINGTON, D.C. 20231

PRELIMINARY AMENDMENT

Please enter the following amendment in the above-referenced patent application:

In the Specification:

At page 9, line 35, please replace the term "DH5 \square " with --DH5 α --.

At page 12, line 12, please replace the term "DH5 \square " with --DH5 α --.

At page 13, line 35, please replace the term "DH5 \square " with --DH5 α --.

At page 25, please insert the following complete citation after line 8: --Bannantine, J.P., et al. (1998) *Infect. Immun.* 66:6017-6021.--.

REMARKS

By this voluntary amendment, the Specification of the application has been amended solely to correct administrative and typographical errors and omissions. The *E. coli* strain DH5 α is well known, and the corrections to this term are made only to correct a printing error. Support for the insertion of the Bannantine *et al.* (1998) citation can be found at page

PATENT

14, line 17, which provides sufficient information to locate this article. Applicants believe this amendment adds no new matter to the application.

Respectfully submitted,

KLARQUIST SPARKMAN CAMPBELL
LEIGH & WHINSTON, LLP

By

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CHLAMYDIA PROTEINS AND THEIR USES

I. FIELD OF THE INVENTION

The present invention relates to the detection of *Chlamydia* and to the diagnosis, treatment 5 and prevention of *Chlamydia* infections in animals.

II. BACKGROUND

Chlamydiae are obligate intracellular bacterial pathogens with a unique biphasic life cycle. They appear as two distinct cellular types, a small dense cell or elementary body (EB) that is 10 enclosed in a rigid bacterial cell wall, and a larger metabolically active reticulate body (RB). The EB is resistant to physical disruption and is infectious, whereas the RB is more fragile and only exists inside cells. The *Chlamydia* life cycle begins with the attachment of the EB form to the host cell which is followed by endocytosis into a nascent vacuole, also called an "inclusion membrane."

15 After EB attachment and entry, replication of the EB form produces RB forms that continue to grow within the vacuole. By 72 hour post-infection, this growth phase is terminated when the RBs condense, and reorganize back to EBs. The lysis of the host cell results in release of EBs to infect new host cells. The difficulties in working with *Chlamydiae* center on the obligate intracellular requirement for growth and the fact that no adequate genetic engineering methods have been developed for this organism.

20 The genus *Chlamydia* includes two species that are primarily associated with human disease: *C. trachomatis* and *C. pneumoniae*. *C. trachomatis* causes trachoma, an eye disease that is the leading cause of preventable infectious blindness worldwide with an estimated 500 million cases of active trachoma worldwide. *C. trachomatis* also causes a sexually transmitted chlamydial disease which is very common worldwide. *C. trachomatis* also causes lymphogranuloma 25 venereum, a debilitating systemic disease characterized by lymphatic gland swelling. The most serious sequelae of chlamydial genital infections of females include salpingitis, pelvic inflammatory disease, and ectopic pregnancy. In the US alone, it is estimated that over 4 million new sexually transmitted *C. trachomatis* infections occurred in 1990, leading to over four billion dollars in direct and indirect medical expenses. The World Health Organization estimates that 89 30 million new cases of genital *Chlamydia* occurred worldwide in 1995 (Peeling and Brunham, 1996).

C. pneumoniae causes respiratory diseases including so called walking pneumonia, a low-grade disease such that the infected person frequently fails to obtain treatment and remains in the community as an active, infectious carrier. *C. pneumoniae* is currently of interest because of its strong epidemiological association with coronary artery disease, and there is also some evidence to link it with multiple sclerosis.

35 Of the other disease-causing species of *Chlamydia*, *Chlamydia psittaci* and *Chlamydia pecorum* are primarily pathogens of wild and domestic animals, but these species may infect

humans accidentally. *C. psittaci* is acquired through respiratory droplet infection and is considered an occupational health hazard for bird fanciers and poultry workers.

There is tremendous interest in the identification of candidate antigens for protection against chlamydial disease. While a prior infection with *C. trachomatis* will protect against a subsequent challenge by the same strain, indicating a protective component that stimulates the host immune response, most serious chlamydial diseases are exacerbated by an overaggressive anti-chlamydial immune response. Antigens recognized in the context of an infection appear to elicit a protective response whereas immunization with purified, killed (EB form) *Chlamydia* results in an immunopathological response. Therefore for the purposes of vaccine development, one needs to find epitopes that confer protection, but do not contribute to pathology. It is an object of this invention to provide *Chlamydia* polypeptides for use as vaccines that induce a protective immune response without inducing the pathological response caused by the antigens associated with the EB form of *Chlamydia*. Such immunostimulatory peptides will be useful in the treatment, as well as in the diagnosis, detection and prevention of Chlamydial infections.

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III. SUMMARY OF THE INVENTION

The present invention includes the use of *Chlamydia* proteins that show enhanced expression in the reticulate body (RB) stage relative to the elementary body (EB) stage of the *Chlamydia* life cycle. These proteins are not present at detectable levels in the EB form using current immunological techniques and are thus said to be "infection-specific." Certain of these infection-specific proteins are found in the inclusion membrane of the infected cell, and so have been termed "Inc" proteins. These include the IncA, IncB, and IncC proteins of *Chlamydia* as described in the present disclosure. The genes that encode the IncA, IncB and IncC proteins are referred to as *incA*, *incB* and *incC* respectively. Other proteins of *Chlamydia* described herein have also been shown by the inventors to be infection-specific, but are not known to be incorporated into the inclusion membrane; these include the p242, TroA, and TroB proteins. The TroA and TroB proteins have been so named because they resemble the Tro proteins of *Treponema pallidum*, which are thought to form part of an ABC transport system.

20

The inventors have shown that the infection-specific *Chlamydia* proteins of the disclosure are recognized by convalescent antisera (i.e., antisera taken from an animal that has recovered from a *Chlamydia* infection) but are not recognized by antisera against the killed EB form of *Chlamydia*. Thus, the proteins are expressed only during active chlamydial infection and are therefore useful as protective antigens. These infection-specific proteins may be used to confer a protective immune response without inducing a pathological effect. Additionally, immuno-fluorescence microscopy and immunoblotting with antisera demonstrated that the infection-specific proteins are present in *Chlamydia*-infected HeLa cells, but are undetectable in purified EBs and absent in uninfected HeLa cells.

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Immunofluorescence microscopy reveals that IncA, IncB and IncC are localized to the inclusion membrane of infected HeLa cells. Reverse-transcription polymerase chain reactions (RT-PCR), northern hybridization data, and restriction analysis revealed that the *incB* and *incC* genes are closely linked and transcribed in an operon. RT-PCR, restriction analysis and sequential Southern hybridizations of *incA* then *incC* to the same filter provided evidence that *incA* is separated from the *incB* and *incC* operon by about 110 kb. The *C. trachomatis* *Tro* genes are not closely linked with the p242 gene.

The present invention includes the nucleotide and amino acid sequences for certain infection-specific proteins from *Chlamydia*. These proteins are p242, TroA, and TroB from *C. trachomatis*, and the IncB, and IncC proteins from *C. psittaci*. The scope of the invention includes fragments of these proteins that may be used in a vaccine preparation or that may be used in a method of detecting *Chlamydia* antibodies. Such fragments may be, for example, 5, 10, 15, 20, 25, or 30 contiguous amino acids in length. They may even encompass the entire protein.

More specifically, the present invention encompasses the purified infection-specific 15 proteins having amino acid sequences as shown in SEQ ID NOS: 2, 4, 6, 10, and 12, amino acid sequences that differ from such sequences by one or more conservative amino acid substitutions, and amino acid sequences that show at least 75% sequence identity with such amino acid sequences.

Then invention also includes isolated nucleic acid molecules that encode a protein as 20 described in the above paragraph, including isolated nucleic acid molecules with nucleotide sequences as shown in SEQ ID NOS: 1,3, 5, 9, and 11.

The present invention also includes a vaccine or immunostimulatory preparation directed against the reticulate body (RB) form of *Chlamydia* comprising one or more purified infection-specific peptides (or portions or fragments thereof, or peptides showing sequence similarity to a portion of such a peptide). Such peptide fragments may be, for example, 5, 10, 15, 20, 25, or 30 contiguous amino acids in length, of the sequence shown in SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, or 18. Peptides used in such a vaccine may even encompass the entire purified peptide of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, or 18, a peptide that differs from such a peptide by one or more conservative amino acid substitutions, or a peptide having at least 75% sequence identity 30 with such a peptide. Such vaccine preparations may contain one or more pharmaceutically acceptable excipients, adjuvants or diluents.

The invention additionally encompasses methods for making a vaccine, comprising combining a pharmaceutically acceptable excipient with a peptide described herein. Also included is a method of vaccination comprising administering a vaccine as described herein to a mammal.

35 The present invention also provides a method for the diagnostic use of the disclosed purified infection-specific peptides, for instance by use in a diagnostic assay to detect the presence of infection-specific antibodies in a medical specimen, in which antibodies bind to the *Chlamydia* peptide and indicate that the subject from which the specimen was removed was previously

exposed to *Chlamydia*. Such a method may comprise: (i) supplying a biological sample, such as blood from an animal, that is suspected to contain infection-specific anti-*Chlamydia* antibody, (ii) contacting the sample with at least one infection-specific *Chlamydia* peptide described herein, such that a reaction between the peptide and the infection-specific anti-*Chlamydia* antibody gives rise to a detectable effect, such as a chromogenic conversion; and (iii) detecting this detectable effect.

The present invention also provides a method of using antibodies that bind specifically with the disclosed proteins for detection of infection-specific *Chlamydia* antigen, indicating the presence of *Chlamydia* in the RB stage as distinct from the EB stage. For instance, the relevant infection-specific antibodies may be used to provide specific binding in an Enzyme Linked 10 Immunosorbant Assay (ELISA) or other immunological assay wherein the antibody *Fc* portion is linked to a chromogenic, fluorescent or radioactive molecule and the *Fab* portion specifically interacts with, and binds to, an infection-specific protein. Such a method may comprise: (i) supplying a biological sample from an animal suspected to contain an infection-specific *Chlamydia* antigen, and (ii) contacting the sample with at least one infection-specific anti-*Chlamydia* antibody, 15 such that a reaction between the antibody and the infection-specific *Chlamydia* protein gives rise to a detectable effect; and (iii) detecting this detectable effect.

Other aspects of the present invention include the use of probes and primers derived from the nucleotide sequences that encode infection-specific peptides, to detect the presence of *Chlamydia* nucleic acids in medical specimens. Such probes and primers may be nucleotide 20 fragments, of, for example, 15, 20, 25, 30 or 40 contiguous nucleotides of the sequence shown in SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, or 17.

An additional aspect of the invention is a method of treating a *Chlamydia* infection by directing a therapeutic agent against a specific target, where the target is chosen from an infection specific protein of *Chlamydia*, a gene that encodes an infection-specific protein of *Chlamydia*, and 25 an RNA transcript that encodes an infection-specific protein of *Chlamydia*, wherein the therapeutic agent interacts with said target to affect a reduction in pathology.

These and other aspects of the invention will become more apparent from the following description.

30 IV. SEQUENCE LISTING

SEQ ID NO:1 shows a nucleic acid sequence encoding the p242 *C. trachomatis* protein, with deduced primary amino acid sequence also shown.

SEQ ID NO:2 shows the amino acid sequence of the p242 *C. trachomatis* protein.

SEQ ID NO:3 shows a nucleic acid sequence encoding the TroA *C. trachomatis* protein, 35 with deduced primary amino acid sequence also shown.

SEQ ID NO:4 shows the amino acid sequence of the TroA *C. trachomatis* protein.

SEQ ID NO:5 shows a nucleic acid sequence encoding the TroB *C. trachomatis* protein, with deduced primary amino acid sequence also shown.

SEQ ID NO:6 shows the amino acid sequence of the TrkB *C. trachomatis* protein.

SEQ ID NO:7 shows a nucleic acid sequence encoding the IncA *C. psittaci* protein, with deduced primary amino acid sequence also shown.

SEQ ID NO:8 shows the amino acid sequence of the IncA *C. psittaci* protein.

5 SEQ ID NO:9 shows a nucleic acid sequence encoding the IncB *C. psittaci* protein, with deduced primary amino acid sequence also shown.

SEQ ID NO:10 shows the amino acid sequence of the IncB *C. psittaci* protein.

SEQ ID NO:11 shows a nucleic acid sequence encoding the IncC *C. psittaci* protein, with deduced primary amino acid sequence also shown.

10 SEQ ID NO:12 shows the amino acid sequence of the IncC *C. psittaci* protein.

SEQ ID NO:13 shows a nucleic acid sequence encoding the IncA *C. trachomatis* protein, with deduced primary amino acid sequence also shown.

SEQ ID NO:14 shows the amino acid sequence of the IncA *C. trachomatis* protein.

15 SEQ ID NO:15 shows a nucleic acid sequence encoding the IncB *C. trachomatis* protein, with deduced primary amino acid sequence also shown.

SEQ ID NO:16 shows the amino acid sequence of the IncB *C. trachomatis* protein.

SEQ ID NO:17 shows a nucleic acid sequence encoding the IncC *C. trachomatis* protein, with deduced primary amino acid sequence also shown.

SEQ ID NO:18 shows the amino acid sequence of the IncC *C. trachomatis* protein.

20 SEQ ID NO:19 shows the upstream oligonucleotide used to amplify the *C. psittaci incC* ORF.

SEQ ID NO:20 shows the downstream oligonucleotide used to amplify the *C. psittaci incC* ORF.

25 SEQ ID NO:21 shows the upstream oligonucleotide used to amplify the *C. psittaci incB* ORF.

SEQ ID NO:22 shows the downstream oligonucleotide used to amplify the *C. psittaci incB* ORF.

SEQ ID NO:23 shows the upstream oligonucleotide used to amplify the *C. psittaci incA* ORF.

30 SEQ ID NO:24 shows the downstream oligonucleotide used to amplify the *C. psittaci incA* ORF.

V. DESCRIPTION OF THE INVENTION

A. DEFINITIONS

35 Particular terms and phrases used herein have the meanings set forth below.

"EB" refers to the Elementary Body, an environmentally refractile and largely metabolically dormant form of *Chlamydia* that is infectious and is presented as a small dense body enclosed by a bacterial cell wall.

5 "RB" refers to the Reticulate Body, a metabolically active form of *Chlamydia* that is not infectious, and exists only within a host cell, being very fragile, often branched, and appearing larger and less dense than the EB.

"Infection-specific" refers to a protein that shows enhanced expression in the RB form of *Chlamydia* compared to the EB form. Infection-specific proteins are not necessarily absent from the EB form, but they are significantly more common in the RB form than in the EB form.

10 "infection-specific antibody" is an antibody that binds specifically to an infection-specific protein.

"Biological sample" refers to any sample of biological origin including, but not limited to a blood sample, a plasma sample, a mucosal smear or a tissue sample.

15 "Isolated" An isolated nucleic acid has been substantially separated or purified away from other nucleic acid sequences in the cell of the organism in which the nucleic acid naturally occurs, i.e., other chromosomal and extrachromosomal DNA and RNA. The term "isolated" thus encompasses nucleic acids purified by standard nucleic acid purification methods. The term also embraces nucleic acids prepared by recombinant expression in a host cell as well as chemically synthesized nucleic acids.

20 "Probes" and "primers." Nucleic acid probes and primers may readily be prepared based on the nucleic acid sequences provided by this invention. A "probe" comprises an isolated nucleic acid attached to a detectable label or reporter molecule. Typical labels include radioactive isotopes, ligands, chemiluminescent agents, and enzymes.

25 "Primers" are short nucleic acids, typically DNA oligonucleotides 15 nucleotides or more in length, which are annealed to a complementary target DNA strand by nucleic acid hybridization to form a hybrid between the primer and the target DNA strand, then extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR) or other nucleic-acid amplification methods known in the art.

30 Probes and primers as used in the present invention typically comprise at least 15 nucleotides of the nucleic acid sequences that are shown to encode infection-specific proteins. In order to enhance specificity, longer probes and primers may also be employed, such as probes and primers that comprise at least 20, 30 or 40 consecutive nucleotides of the disclosed nucleic acid sequences.

35 Methods for preparing and using probes and primers are well known in the art and are described in, for example Sambrook et al. (1989); Ausubel et al., (1987); and Innis et al., (1990). PCR primer pairs can be derived from a known sequence, for example, by using computer

programs intended for that purpose such as Primer (Version 0.5, 1991, Whitehead Institute for Biomedical Research, Cambridge, MA).

"Conservative amino acid substitutions" are those substitutions that least interfere with the properties of the original protein, i.e., the structure and especially the function of the protein is conserved and not significantly changed by such substitutions. The table below shows amino acids which may be substituted for an original amino acid in a protein and which are regarded as conservative substitutions.

Original Residue	Conservative Substitution
Ala	Ser
Arg	Lys
Asn	gln, his
Asp	Glu
Cys	Ser
Gln	Asn
Glu	Asp
Gly	Pro
His	asn, gln
Ile	leu, val
Leu	ile, val
Lys	arg, gln, glu
Met	leu, ile
Phe	met, leu, tyr
Ser	Thr
Thr	Ser
Trp	Tyr
Tyr	trp, phe
Val	ile, leu

Conservative substitutions generally maintain (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain.

The substitutions which in general are expected to produce the greatest changes in protein properties will be non-conservative, for instance changes in which (a) a hydrophilic residue, e.g., seryl or threonyl, is substituted for (or by) a hydrophobic residue, e.g., leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g., lysyl, arginyl, or histadyl, is substituted for (or by) an electronegative residue, e.g., glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine.

"Sequence identity" The similarity between two nucleic acid sequences, or two amino acid sequences is expressed in terms of the level of sequence identity shared between the sequences. Sequence identity is typically expressed in terms of percentage identity; the higher the percentage, the more similar the two sequences are. Variants of naturally occurring infection-specific peptides useful in the present invention are typically characterized by possession of at least 50% sequence identity counted over the full length alignment with the amino acid sequence of a

naturally occurring infection-specific peptide when aligned using BLAST 2.0.1 (Altschul et al., 1997). For comparisons of amino acid sequences of greater than about 30 amino acids, the BLAST 2 analysis is employed using the blastp program set to default parameters (open gap = 11, extension gap = 1 penalty, gap x dropoff = 50, expect = 10, word size = 3, filter on), and using 5 the default BLOSUM62 matrix (gap existence cost = 11, per residue gap cost = 1, lambda ratio = 0.85). When aligning short peptides (fewer than around 30 amino acids), the alignment should be performed using the Blast 2 sequences function, employing the PAM30 matrix (gap existence cost = 9, per residue gap cost = 1, lambda ratio = 0.87). Proteins with even greater similarity to the reference sequences will show increasing percentage identities when assessed by this method, 10 such as at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, or at least 95% sequence identity. The NCBI Basic Local Alignment Search Tool (BLAST) (Altschul et al., 1990) is available from several sources, including the National Center for Biotechnology Information (NCBI, Bethesda, MD) and on the Internet, for use in connection with the sequence analysis programs blastp, blastn, blastx, tblastn and tblastx. It can be accessed at 15 <http://www.ncbi.nlm.nih.gov/BLAST/>. A description of how to determine sequence identity using this program is available at http://www.ncbi.nlm.nih.gov/BLAST/blast_help.html.

Similarly, when comparing nucleotides, blastn may be used with default settings (rewards for match = 1, penalty for mismatch = -2, open gap = 5, extension gap = 2 penalty, gap x dropoff = 50, expect = 10, word size = 11, filter on), with the default BLOSUM62 matrix (as above). Variants of naturally occurring infection-specific nucleic acid sequences useful in the 20 present invention are typically characterized by possession of at least 50% sequence identity counted over the full length alignment with the nucleic acid sequence of a naturally occurring infection-specific ORF when aligned using BLAST 2.0.1. Useful nucleic acids may show even greater percentage identity, and may, for example, possess at least 55%, at least 65%, at least 75%, at least 80%, at least 85%, at least 90%, or at least 95% sequence identity naturally 25 occurring infection-specific ORF.

"Operably linked" A first nucleic acid sequence is "operably" linked with a second nucleic acid sequence when the first nucleic acid sequence is placed in a functional relationship with the nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence 30 if the promoter affects the transcription or expression of the coding sequence. Generally, operably linked DNA sequences are contiguous and, where necessary to join two protein coding regions, in the same reading frame.

"Recombinant" A recombinant nucleic acid is one that has a sequence that is not naturally occurring or has a sequence that is made by an artificial combination of two otherwise separated 35 segments of sequence. This artificial combination is often accomplished by chemical synthesis or, more commonly, by the artificial manipulation of isolated segments of nucleic acids, e.g., by genetic engineering techniques.

"Stringent Conditions" Stringent conditions, in the context of nucleic acid hybridization, are sequence-dependent and are different under different environmental parameters. Generally, stringent conditions are selected to be about 5 degrees to 20 degrees lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Conditions for nucleic acid hybridization and calculation of stringencies can be found in Sambrook et al. (1989), pages 9.49-9.55. Typical high stringency hybridization conditions (using radiolabeled probes to hybridize to nucleic acids immobilized on nitrocellulose filter) may include, for example, wash conditions of 0.1 X SSC, 0.5% SDS at a wash temperature of 68°C.

When referring to a probe or primer, the term "specific for (a target sequence)" indicates that the probe or primer hybridizes under high-stringency conditions substantially only to the target sequence in a given sample comprising the target sequence.

"Purified" A purified peptide is a peptide that has been extracted from the cellular environment and separated from substantially all other cellular peptides. As used herein, the term peptide includes peptides, polypeptides and proteins. In certain embodiments, a purified peptide is a preparation in which the subject peptide comprises 50% or more of the protein content of the preparation. For certain uses, such as vaccine preparations, even greater purity may be preferable.

"Immunostimulatory peptide" as used herein refers to a peptide that is capable of stimulating a humoral or antibody-mediated immune response when inoculated into an animal.

"Vaccine" A vaccine is a composition containing at least one immunostimulatory peptide which may be inoculated into an animal with the intention of producing a protective immunological reaction against a certain antigen. The antigen to be protected against may be, for instance, an infectio-specific antigen of *Chlamydia*.

B. ISOLATION OF INFECTION SPECIFIC CHLAMYDIA POLYPEPTIDES AND IDENTIFICATION OF GENES ENCODING THESE POLYPEPTIDES

30 1. ISOLATION OF IncA, IncB AND IncC

Bacterial strains. *Chlamydia* (*C. psittaci* strain GPIC or *C. trachomatis* LGV-434, ser. L2) was cultivated in HeLa 229 cells using standard methods (Caldwell et al., 1981). Purified *Chlamydiae* were obtained using Renografin (E. R. Squibb & Sons, Inc., Princeton, N.J.) density gradient centrifugation. *Escherichia coli* DH5 δ (Bethesda Research Laboratories, Inc., Gaithersburg, Md.) was used as the host strain for transformations with recombinant DNA. *E. coli* XL1-Blue MRF' (Stratagene, La Jolla, Calif.) was used as the host strain for infection with lambda ZAPII phage vector. *E. coli* SOLR (Stratagene) was used as the host strain for infection with *in vivo* excised filamentous lambda ZAPII.

Antisera. MBP (Maltose Binding Protein)-Inc fusion proteins were used as antigens for the production of mono-specific antibody reagents in Hartley strain guinea-pigs. The protein was diluted to 100 µg/ml⁻¹ sterile saline and mixed with the Ribi Trivalent Adjuvant (Ribi Immunochem.). The antigen/adjuvant emulsion was administered to anaesthetized guinea-pigs
5 using a procedure provided by the manufacturer. Sera were collected 14 days after secondary and tertiary immunizations. Control antisera were produced by immunizing guinea-pigs with adjuvant alone, or with adjuvant plus purified maltose-binding protein.

Convalescent guinea-pig antisera, antisera against live EBs, and antisera against formalin-fixed EBs were produced using standard methods (Rockey and Rosquist, 1994 and Rockey et al.,
10 1995).

C. psittaci library construction and screening. For the *incB* and *incC* genes, *C. psittaci* strain GPIC DNA was extracted using a genomic DNA extraction kit (Qiagen) with one modification; dithiothreitol (5mM) was added to the suspension buffer to assist EB lysis. DNA was partially digested with *Tsp*509I and ligated to *Eco*R1 digested λ-ZAPII phage arms
15 (Stratagene). The ligation was packaged in vitro with Gigapack extracts according to the manufacturer's instructions (Stratagene). Recombinant phage were plated on *E. coli* XL-1 Blue at densities of approximately 10⁴ PFU/150-mm (diameter) plate. Following a nine hour incubation to allow development of the plaques, the plates were sequentially overlaid with nitrocellulose disks and the resulting lifts were processed for immunoblotting with convalescent antisera and antisera to fixed EBs. Of approximately 8,000 plaques, 18 had reactivity with the convalescent sera but not sera generated against EBs. One of these was subcloned into pBluescript SK(-) phagemid by *in*
20 *vitro* excision in the *E. coli* SOLR strain (Stratagene) and designated pBS200-7.

For the *incA* gene, genomic DNA from *C. psittaci* strain GPIC was partially digested with *Sau*3A, size-selected (2-8 kb) by electrophoresis through low-melting-temperature agarose,
25 and blunt-ended with T4 DNA polymerase. This DNA was ligated to an *Eco*R1/*Not*I adapter (Life Technologies), kinased, and ligated to *Eco*R1-digested Lambda ZAP II vector (Stratagene Cloning Systems). Recombinants were packaged (Lambda Gigapack Gold, Stratagene) and used to infect *E. coli* XL1-Blue (Stratagene). Plaques were allowed to develop for 4 h at 37°C. Nitrocellulose filters laden with 10 mM IPTG (US Biochemical Corp.) were placed onto the plaques and
30 incubated for an additional 4 h at 37°C. These filters were removed and placed into a blocking solution consisting of PBS (150 mM NaCl, 10 mM NaPO₄, pH7.2) plus 0.1% Tween-20 (TPBS) and 2% BSA-TPBS. Filters were incubated for 1 h, rinsed twice in TPBS, and incubated overnight in convalescent-guinea-pig sera diluted 1:100 in BSA-TPBS. After three washes in TPBS, the filters were incubated for 1 h in ¹²⁵I-staphylococcal protein A (New England Nuclear)
35 diluted to approx. 124 nCi/ml⁻¹ in BSA-TPBS. Filters were again washed three times in TPBS and positive plaques were detected by exposure of the dried filters to autoradiography film overnight at room temperature. Positive clones were picked and plaque-purified. pBluescript-SK- plasmids

containing the chlamydial genes of interest were recovered from the purified bacteriophage using ExAssist filamentous bacteriophages (Stratagene).

Identification of antigens recognized by convalescent antisera. Recombinant plaques were identified that showed reactivity with convalescent (anti-RB) antisera, but not with anti-EB serum. The purified recombinant phage were converted into pBluescriptII SK plasmid by *in vivo* excision and recircularization and these recombinant DNAs were used to transform *E. coli*. SDS-PAGE and immunoblot analysis of lysates of these recombinant *E. coli* showed that each expressed one or more proteins that reacted with convalescent antisera but not with the EB serum.

DNA Cloning and fusion protein production. The plasmid pJC2 contains a 5.0 kb 10 *Eco*RI GPIC genomic fragment cloned into the pZEro2.1 vector (Invitrogen). To construct pJC2, the *incC* ORF sequence was 32 P-radiolabeled using random priming (Gibco-BRL) and used to probe *Eco*RI cut GPIC genomic DNA fragments separated by agarose gel electrophoresis. Fragments in the size range of the positive signal were excised from the gel and purified by Gene-Clean (Bio101). The gel-purified fragments were used in a ligation along with *Eco*RI-digested 15 pZEro2.1. Kanamycin resistant colonies were screened by colony hybridization with radiolabeled *incC*.

MBP fusions of the five ORFs present in pJC2 were produced using the pMAL-C2 vector (New England Biolabs). The reading frame of *incC*, with the exception of the first four codons, was amplified using *Pwo* polymerase (Boehringer Mannheim) and pBS200-7 as the template. The 20 upstream and downstream oligonucleotides for this amplification were
5'-AGAACCGATTAACTCCAGCG-3' (SEQ ID NO: 19) and
5'-GCGCGGATCCTTAAATGTCCGGTAGGCCTAG-3' (SEQ ID NO: 20), respectively. The vector was digested with *Xmn*I and *Bam*H1, and the amplification product was digested with *Bam*H1. Ligation of these products resulted in an in-frame fusion between the *malE* gene in the 25 vector and the *incC* reading frame from pBS200-7. The stop codon for this construction is provided by the insert. Following ligation, the products were transformed into *E. coli* strain HD5D. The resulting fusion protein (MBP/IncC) was overexpressed and purified by maltose affinity chromatography using an amylose resin supplied by New England Biolabs.

The same approach was used for production of the MBP/IncB fusion protein. The 30 sequence encoding the N-terminal 101 amino acids of the IncB ORF was PCR amplified using the oligonucleotides
5'-ATGTCAACAAACACCAGCATCTTC-3' (SEQ ID NO: 21) and
5'-GCGCGGATCCTTAATTAGTGCCTCTGGATTAGG-3' (SEQ ID NO: 22).

The purified MBP/IncB and MBP/IncC fusion proteins were used as antigen for the 35 production of monospecific antibody in Hartley strain guinea-pigs by standard methods (Rockey et al., 1995). Inserts in each construct were confirmed by DNA sequencing.

For IncA, a maltose-binding protein/IncA fusion protein was produced using the pMAL-C2 vector system from New England Biolabs. The reading frame of *incA* shown in Fig. 1, with the exception of the initiator ATG, the *incA* ORF was amplified using Vent DNA polymerase (New England Biolabs) and plasmid pGP17 as template. The upstream and downstream oligo-
5 nucleotides for this amplification were

5'-CGCAGTACTGTATCCACAGACAAC-3' (SEQ ID NO: 23) and

5'-GTCGGATCGAGAAACTCTCCATGCC-3' (SEQ ID NO: 24), respectively. The

vector was digested with *Xmn*I and *Bam*H1, and the amplification product was digested with *Scal*I and *Bam*H1. Ligation of these products resulted in an in-frame fusion between the *malE* gene in
10 the vector and the *incA* reading frame from pGP17. The stop codon for this construction is provided by the insert. Following ligation, the products were transformed into *E. coli* strain DH5 α . The resulting fusion protein (MBP/IncA) was overexpressed and purified by maltose affinity chromatography using amylose resin (New England Biolabs).

15 MBP/IncA was used as antigen for the production of mono-specific antibody reagents in Hartley strain guinea-pigs.

20 **DNA sequencing and sequence analysis.** The pBS200-7 and pJC2 genomic clones as well as the MBP fusions were sequenced with the *Taq* DyeDeoxy Terminator Cycle Sequencing Kit (Perkin Elmer/Applied Biosystems Division). Several internal primers were designed to sequence further into the cloned inserts. Sequence assembly was performed using AssemblyLIGN software and sequence analysis was performed with MacVector software (International Biotechnologies Incorporated). Hydrophilicity profiles were determined using the Kyte-Doolittle scale (Kyte and Doolittle, 1982) with a window of 7. Deduced amino acid sequences were compared with the database using the BLAST program (on default settings) available from the National Center for Biotechnology Information on the world wide web. The entire nucleotide
25 sequence of the pJC2 insert was deposited in the GenBank/EMBL Nucleotide Sequence Data Library, under accession number AF017105.

30 For *incA*, nucleotide sequencing was conducted using the Sequences system (US Biochemical) with the M13 forward and reverse primers, and internal primers synthesized on an Milligen/Bioscience Cyclone Plus DNA synthesizer. Computer analyses were conducted using the MacVector Sequence Analysis Software (International Biotechnologies Incorporated). Hydrophilicity profiles were determined using the Kyte-Doolittle scale (Kyte and Doolittle, 1982) with a window of 7. Secondary-structure predictions were generated using a combination of the Chou-Fasman and Robson-Garnier methods (Robson and Suzuki, 1976; Chou and Fasman, 1978). Deduced amino acid sequences were compared with those in the EMBL and GenBank databases
35 using the BLASTP program available from the National Center for Biotechnology Information.

Electrophoresis and immunoblotting. Polyacrylamide gel electrophoresis (PAGE) was conducted using standard methods (Rockey and Rosquist, 1994). Immunoblotting was performed using standard methods (Rockey et al., 1995).

5 **Immunofluorescence studies.** *Chlamydiae* grown in HeLa cells on sterile glass coverslips were fixed for microscopy one of two ways. Cells were either incubated in methanol for 5 minutes, or in the combination fixative periodate-lysine-parafomaldehyde (PLP) for three hours at room temperature followed by permeabilization with 0.05% saponin (Brown and Farquhar, 1989). Immunostaining of the fixed coverslips was performed according to standard methods (Rockey et al., 1995) and visualized under a Nikon Microphot FXA microscope using the 10 63x objective and oil immersion.

RT-PCR analysis. RNA for RT-PCR analysis was extracted from approximately 2×10^{14} 15 *C. psittaci*-infected cells. A Qiagen column was used for extraction and purification according to the manufacturer's instructions (Qiagen). RQ1 RNase DNase (Promega) was used to ensure removal of contaminating genomic DNA. cDNA was prepared by incubating 1.5 μ g of RNA, 2.5 μ M of the reverse oligonucleotide primer, and AMV reverse transcriptase (Promega) for 1 hour at 42°C in sodium pyrophosphate buffer, according to the manufacturer's instructions. PCR reactions were carried out using 1 μ l of the cDNA reaction, 1.25 μ M of each oligonucleotide primer, and *Pwo* polymerase (Boehringer Mannheim). Each RT-PCR reaction was accompanied by a positive control reaction that utilized the same primer set and 10 ng of *C. psittaci* genomic 20 DNA, and a negative control reaction in which 1 μ l of the same RNA preparation was used as template in the PCR reaction. A control primer set located within the *incC* gene was also used as an RT-PCR control.

Identification of *incA*, *incB* and *incC* genes of *C. trachomatis*. The nucleotide sequence information obtained for the *incA*, *incB* and *incC* of *C. psittaci* (above) was used, with standard 25 methods, to identify the *inc* gene orthologues of *C. trachomatis*. Probes were made that corresponded to the 3' and 5' ends of the *C. psittaci inc* open reading frames. Standard PCR amplification (as above) was used, with the *C. trachomatis* genome as a template, to amplify the corresponding *C. trachomatis* nucleotide sequence. The amplified DNA was then sequenced, using standard methods.

30

2. ISOLATION OF p242, TroA AND TroB

Bacterial strains. *C. trachomatis* LGV-434, serotype L2, was cultivated in HeLa 229 cells using standard methods (Caldwell et al., 1981). Purified *chlamydiae* were obtained using Renografin (E. R. Squibb & Sons, Inc., Princeton, N.J.) density gradient centrifugation (Hackstadt et al., 1992). *Escherichia coli* DH5 α (Bethesda Research Laboratories, Inc., Gaithersburg, Md.) 35 was used as the host strain for transformations with recombinant DNA. *E. coli* XL1-Blue MRF' (Stratagene, La Jolla, Calif.) was used as the host strain for infection with lambda ZAPII phage

vector. *E. coli* SOLR (Stratagene) was used as the host strain for infection with *in vivo* excised filamentous lambda ZAPII.

Antisera. Two Cynomolgus monkeys (*Macaca fascicularis*) were anaesthetized and infected urethrally with *C. trachomatis* EBs. Each monkey was infected twice and allowed to recover between infections. Symptoms of infection were monitored over time. Antisera from infected monkeys were tested for reactivity to *Chlamydia* by ELISA (Su et al., 1990).

Sera were collected every two weeks and anti-chlamydial titers were determined. These animals showed mild clinical signs of disease which cleared spontaneously. A second challenge was then administered. Sera were collected from these animals and used to probe a *C. trachomatis* expression library as discussed below. As a control, Guinea Pigs were immunized with killed *C. trachomatis* of the EB form. Sera from these animals were obtained and also used to probe the *C. trachomatis* expression library.

C. trachomatis library construction and immunoscreening. A *C. trachomatis* genomic library was constructed with the lambda ZAPII vector as described above for *C. psittaci*.

Approximately 15,000 plaques were plated, transferred to nitrocellulose filters (Schleicher and Schuell, Keene, N.H.) in duplicate, and probed with the monkey convalescent antiserum and with Guinea Pig serum against killed EBs (Bannantine et al., 1998). Plaques that reacted only with the monkey convalescent antisera were selected for further study.

Identification of antigens recognized by convalescent antisera. Four positive recombinant plaques were identified that showed reactivity with convalescent antisera but not with anti-EB serum. The purified recombinant phage were converted into pBluescriptII SK plasmid by *in vivo* excision and recircularization and these recombinant DNAs (pCt1, pCt2, pCt3 and pCt4) were used to transform *E. coli*. SDS-PAGE and immunoblot analysis of lysates of these recombinant *E. coli* showed that each expressed one or more proteins that reacted with convalescent (anti-RB) antisera but not with the anti-EB antiserum. Two of the recombinants clones, pCt2 and pCt3, expressed an identical 19.9 kDa protein (p242). The pCt4 recombinant expressed two different proteins of approximately 32 kDa each that are strongly recognized by convalescent antisera (TroA and TroB).

30 C. SEQUENCE ANALYSIS

Sequence analysis of pCt1, 2, and 3 revealed overlapping inserts with only one open reading frame (ORF) common in all three. This ORF encodes an approximately 19.9 kDa protein (p242) that shows no similarity to other known proteins. The nucleotide sequence encoding *C. trachomatis* p242, and the amino acid sequence of the protein are shown in SEQ ID NOS:1 and 2, respectively.

The insert in pCt4 contains two complete ORFs which code for two proteins, each of approximately 32kDa (TroA and TroB) that show some homology with proteins from *Treponema*

pallidum. The nucleotide sequences encoding the 32 kDa proteins (TroA and TroB) and the amino acid sequences of these proteins are shown in SEQ ID NOS: 3, 4, 5, and 6.

D. EMBODIMENTS OF THE INVENTION

5 The present invention includes the nucleotide and amino acid sequences for certain infection-specific proteins from *Chlamydia*. These proteins are p242, TroA, and TroB from *C. trachomatis*, and the IncB, and IncC proteins from *C. psittaci*. The scope of the invention includes fragments of these proteins that may be used in a vaccine preparation or that may be used in a method of detecting *Chlamydia* antibodies. Such fragments may be, for example, 5, 10, 15,
10 20, 25, or 30 contiguous amino acids in length, or may even encompass the entire protein.

The present invention also encompasses the use of infection-specific proteins of *Chlamydia*, and the use of nucleotides encoding such proteins. Infection-specific proteins include the IncA, IncB and IncC proteins of *C. psittaci*, the IncA, IncB and IncC proteins of *C. trachomatis*, and the TroA, TroB, and p242 proteins of *C. trachomatis*. The inventors have shown
15 that these proteins are infection-specific by using immunological techniques such as immunofluorescence microscopy and immunoblotting.

The present invention includes a vaccine against chlamydial infections comprising infection-specific proteins or fragments of these proteins or proteins that are homologous or show substantial sequence similarity to these proteins. In one embodiment, one or more purified
20 infection-specific proteins may be mixed with a pharmaceutically acceptable excipient to produce a vaccine that stimulates a protective immunological response in an animal. In one embodiment the vaccine may be administered intra-muscularly or sub-cutaneously or intravenously. In another embodiment, the vaccine may be administered by inoculation into or onto the mucous membranes of the subject animal. For example, the vaccine may be administered urethrally or genitally as a
25 liquid or in the form of a pessary. In another embodiment, it may be administered to the mucosa of the lungs as a spray or vapor suspension.

Since at least three amino acids are required to produce an antigenic epitope, the vaccine should comprise at least three consecutive amino acids, preferably at least five consecutive amino acids, and may comprise at least 10, 15, 25, 30, 40, or 45 consecutive amino acids of the
30 infection-specific proteins as shown in SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, and 18.

The vaccine of the invention may be used to inoculate potential animal targets of any of the chlamydial diseases including those caused by *C. psittaci*, *C. trachomatis*, *C. pneumoniae* or *C. pecorum*. Indeed the vaccine of the invention may be used to inoculate animals against any disease that shows immunological cross-protection as a result of exposure to infection-specific
35 *Chlamydia* antigen.

Vaccines of the present invention can include effective amounts of immunological adjuvants known to enhance an immune response (e.g., alum). The protein or polypeptide is present in the vaccine in an amount sufficient to induce a protective immune response whether

through humoral or cell mediated pathways or through both. Such a response protects the immunized animal against chlamydial infections specifically by raising an immune response against the Reticulate Body form of *Chlamydia*. Protective antibodies may be elicited by a series of two or three doses of the antigenic vaccine given about two weeks apart.

5 The present invention also teaches a method of making a vaccine against chlamydial infections. The method of making the vaccine comprises providing a pure (or substantially pure) infection-specific chlamydial peptide or portion thereof, and mixing the peptide with a pharmacologically acceptable excipient or adjuvant. Adjuvants may include commonly used compounds such as alum. Additionally, the vaccines may be formulated using a peptide according
10 to the present invention together with a pharmaceutically acceptable excipient such as water, saline, dextrose and glycerol. The vaccines may also include auxiliary substances such as emulsifying agents and pH buffers. Doses of the vaccine administered will vary depending on the antigenicity of the particular peptide or peptide combination employed in the vaccine and characteristics of the animal or human patient to be vaccinated.

15 The infection-specific vaccine of the invention is directed towards not only *C. psittaci*, but against all forms of *Chlamydia* including *C. pneumoniae*, *C. trachomatis* and *C. pecorum*, and the vaccine may comprise not just peptides derived from *C. psittaci*, but also orthologous peptides and fragments of such orthologous peptides from other species of *Chlamydia* and peptides that are substantially similar to such peptides.

20 The present invention also teaches a method of vaccination comprising administering a vaccine formulated as described above to an animal either intravenously, intramuscularly, subcutaneously, by inhalation of a vapor or mist, or by inoculation in the form of a liquid, spray, ointment, pessary or pill into or onto the mucous membranes of the mouth, nose, lungs or urogenital tract or colon.

25 The methods of the invention may be practiced equally with human or non-human animal subjects.

The present invention also teaches a method of detecting *Chlamydia* infection-specific proteins produced by the Reticulate Body form of the organism. In this embodiment, antibodies raised to the infection-specific proteins are used in an immunological assay such as an Enzyme
30 Linked Immunosorbant Assay or Biotin-Avidin assay or a radioimmunoassay or any other assay wherein specific antibodies are used to recognize a specific protein. Such assays may be used to detect both the quantity of proteins present and also the specificity of binding of such proteins. In such an assay, antibodies have attached to them, usually at the *Fc* portion, a detectable label, such as an enzyme, fluorescent marker, a radioactive marker or a Biotin-Avidin system marker that
35 allows detection. A biological sample is provided from an animal that has been putatively exposed to *Chlamydia*. Such a sample may be, for example, whole blood, serum, tissue, saliva or a mucosal secretion. The sample is then contacted with the labeled antibody and specific binding, if any, is detected. Other methods of using infection-specific antibodies to detect infection-specific

antigens that are present in cells or tissues include immunofluorescence, indirect-immunofluorescence and immunohistochemistry. In immunofluorescence, a fluorescent dye is bound directly to the antibody. In indirect-immunofluorescence, the dye is bound to an anti-immunoglobulin. Specific binding occurs between antigen and bound antibody is detected by virtue of fluorescent emissions from the dye moiety. This technique would be particularly useful, for instance, for detection of *Chlamydia* antigen present on a urogenital mucosal smear.

Other techniques, such as competitive inhibition assays may also be used to assay for antigen, and one of ordinary skill in the art will readily appreciate that the precise methods disclosed may be modified or varied without departing from the subject or spirit of the invention taught herein.

The present invention also teaches a method of detection of *Chlamydia* infection-specific antibodies made against the Reticulate Body. In this embodiment a sample is provided from an animal putatively exposed to *Chlamydia* to determine whether the sample contains infection-specific antibodies. Such a sample may be, for example, whole blood, serum, tissue, saliva or a mucosal secretion. This sample is contacted with infection-specific antigens such that the amount and specificity of binding of the antibody may be measured by its binding to a specific antigen. Many techniques are commonly known in the art for the detection and quantification of antigen. Most commonly, the purified antigen will be bound to a substrate, the antibody of the sample will bind via its *Fab* portion to this antigen, the substrate will then be washed and a second, labeled antibody will then be added which will bind to the *Fc* portion of the antibody that is the subject of the assay. The second, labeled antibody will be species specific, i.e., if the serum is from a human, the second, labeled antibody will be anti-human-IgG antibody. The specimen will then be washed and the amount of the second, labeled antibody that has been bound will be detected and quantified by standard methods.

The present invention also teaches a method of treating a *Chlamydial* infection by directing a therapeutic agent against a specific target, such as: (i) an infection-specific protein of *Chlamydia*, (ii) a gene that encodes an infection-specific protein of *Chlamydia* and (iii) an RNA transcript that encodes an infection-specific protein of *Chlamydia*, wherein said therapeutic agent interacts with said target to affect a reduction in pathology.

For example, the present invention teaches a method of treating chlamydial infection wherein antisense technology is used to prevent the expression of infection-specific genes, thereby preventing the pathologies associated these proteins and preventing reproduction of the RB phase of *Chlamydia*. In this embodiment, RNA molecules complementary to transcripts of infection specific genes are introduced into the host cells that contain *Chlamydia*, and by binding to the mRNA transcripts of the infection-specific genes, prevent translation and therefore expression of the infection-specific proteins that are associated with pathogenesis.

The invention may be practiced to produce a vaccine against any species of *Chlamydia*, including *C. psittaci*, *C. pecorum*, *C. trachomatis* and *C. pneumoniae*.

The following examples illustrate various embodiments of the invention.

EXAMPLE 1: Homologous Sequences

The DNA and protein sequences discussed herein are shown in SEQ ID NOS:1-18.

5 These sequences refer to infection-specific proteins and to the DNA sequences that encode these proteins. Although these sequences are from *C. psittaci* and *C. trachomatis*, it would be equally possible to substitute in the present invention, the orthologs of these sequences from other *Chlamydia* species such as *C. pecorum* and *C. pneumoniae*.

Such orthologous sequences may be obtained from the appropriate organisms by isolation
10 of the genome of the organism, digestion with restriction enzymes, separation of restriction fragments by electrophoresis and purification of these fragments and selection of fragments of appropriate size. Identity of the fragments can be confirmed by dot-blot and by standard DNA sequencing techniques. The orthologous sequences in different *Chlamydia* species may also be found by selection of appropriate PCR primers (selected from appropriate regions flanking the
15 *Chlamydia* gene of interest), and the use of these primers in a PCR reaction, using the genome of the particular species of *Chlamydia* of interest as a template, to amplify the ortholog of interest. Such PCR primers would be selected from the flanking regions to allow specific amplification of the target gene. The fragments so obtained could then be run on a gel to check size and sequenced and compared against the known sequences to determine sequence identity.

20 The degree of sequence identity between the infection-specific genes of *C. psittaci* or *C. trachomatis* and their orthologs from *C. pecorum* and *C. pneumoniae*, may be determined by comparing sequences using the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST) as described herein.

Orthologues of interest infection-specific proteins are characterized by possession of at
25 least 50% or greater sequence identity counted over the full length alignment with one of the disclosed amino acid sequences of the *C. psittaci* or *C. trachomatis* infection-specific proteins using gapped blastp set to default parameters (described herein).

EXAMPLE 2: Heterologous Expression of Infection-Specific Antigens

30 Methods for expressing large amounts of protein from a cloned gene introduced into *Escherichia coli* (*E. coli*) may be utilized for the purification of the *Chlamydia* peptides. Methods and plasmid vectors for producing fusion proteins and intact native proteins in bacteria are well known and are described in Sambrook et al. (1989). Such fusion proteins may be made in large amounts, are relatively simple to purify, and can be used to produce antibodies. Native proteins
35 can be produced in bacteria by placing a strong, regulated promoter and an efficient ribosome binding site upstream of the cloned gene. If low levels of protein are produced, additional steps

may be taken to increase protein production; if high levels of protein are produced, purification is relatively easy.

Often, proteins expressed at high levels are found in insoluble inclusion bodies. Methods for extracting proteins from these aggregates are described in chapter 17 of Sambrook et al.

5 (1989). Vector systems suitable for the expression of *lacZ* fusion genes include the pUC series of vectors (Ruther et al. (1983)), pEX1-3 (Stanley and Luzio (1984)) and pMR100 (Gray et al. (1982)). Vectors suitable for the production of intact native proteins include pKC30 (Shimatake and Rosenberg (1981)), pKK177-3 (Amann and Brosius (1985)) and pET-3 (Studiar and Moffatt (1986)).

10 Fusion proteins may be isolated from protein gels, lyophilized, ground into a powder and used as antigen preparations.

Mammalian or other eukaryotic host cells, such as those of yeast, filamentous fungi, plant, insect, amphibian or avian species, may also be used for protein expression, as is well known in the art. Examples of commonly used mammalian host cell lines are VERO and HeLa cells, Chinese hamster ovary (CHO) cells, and WI38, BHK, and COS cell lines, although it will be appreciated by the skilled practitioner that other prokaryotic and eukaryotic cells and cell lines may be appropriate for a variety of purposes, e.g., to provide higher expression, post-translational modification, desirable glycosylation patterns, or other features.

15 Additionally, peptides, particularly shorter peptides, may be chemically synthesized, avoiding the need for purification from cells or culture media. It is known that peptides as short as 3 amino acids can act as an antigenic determinant and stimulate an immune response. Such peptides may be administered as vaccines in ISCOMs (Immune Stimulatory Complexes) as described by Janeway & Travers, Immunobiology: The Immune System In Health and Disease, 13.21 (Garland Publishing, Inc. New York, 1997). Accordingly, one aspect of the present invention includes small peptides encoded by the nucleic acid molecules disclosed herein. Such peptides include at least 5, and may be at least 10, 15, 20, 25, or 30 or more contiguous amino acids of the polypeptide sequences described herein.

20 **EXAMPLE 3: Production of Antibodies Specific for
Infection-Specific Antigens**

25 Antibody against infection-specific antigen is encompassed by the present invention, particularly for the detection of *Chlamydia* infection-specific antigen. Such antibody may be produced by inoculation of an animal such as a guinea-pig or a monkey with infection-specific antigen produced as described above. Such antigen may be a polypeptide as disclosed herein, such as a complete or partial polypeptide from *C. psittaci*, *C. trachomatis*, *C. pneumoniae* or *C. pecorum*. As discussed above, any molecule that can elicit a specific, protective immune response

may be used as a vaccine, but since a minimum of three amino acids are required to do this, a vaccine should comprise at least three amino acids.

The peptide for use in the vaccine of the invention may be naturally derived or may be synthetic such as those synthesized on a commercially available peptide synthesizer. The peptide 5 may also comprise a complete or partial peptide derived from the *C. pneumoniae* or *C. pecorum* infection-specific orthologs of the *C. trachomatis* or *C. psittaci* proteins as set out herein.

In one method of production, a polyclonal antibody is produced by providing a purified peptide which is diluted to 100 micrograms per milliliter in sterile saline and mixed with RiBi 10 Trivalent Adjuvant (RiBi Immunochem Inc). The antigen/adjuvant emulsion is then administered to an anaesthetized guinea pig using a procedure as provided by the manufacturer. Serum is collected 14 days after secondary and tertiary immunizations.

Monoclonal antibody to epitopes of the *Chlamydia* peptides identified and isolated as described can be prepared from murine hybridomas according to the classical method of Kohler and Milstein (1975) or derivative methods thereof. Briefly, a mouse is repetitively inoculated with 15 a few micrograms of the selected purified protein over a period of a few weeks. The mouse is then sacrificed, and the antibody-producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells destroyed by growth of the system on selective media comprising aminopterin, e.g., Hypoxanthene, Aminopterin and Thymidine (HAT) medium. The successfully fused cells are diluted and aliquots 20 of the dilution placed in wells of a microtiter plate where growth of the culture is continued. Antibody-producing clones are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as ELISA, as originally described by Engvall (1980), and derivative methods thereof. Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are 25 described in Harlow and Lane (1988).

An alternative approach to raising antibodies against the *Chlamydia* peptides is to use synthetic peptides synthesized on a commercially available peptide synthesizer based upon the amino acid sequence of the peptides predicted from nucleotide sequence data.

In another embodiment of the present invention, monoclonal antibodies that recognize a 30 specific *Chlamydia* peptide are produced. Optimally, monoclonal antibodies will be specific to each peptide, i.e., such antibodies recognize and bind one *Chlamydia* peptide and do not substantially recognize or bind to other proteins, including those found in uninfected human cells.

The determination that an antibody specifically detects a particular *Chlamydia* peptide is made by any one of a number of standard immunoassay methods; for instance, the western blotting technique (Sambrook et al., 1989). To determine that a given antibody preparation (for instance 35 from a guinea pig) specifically detects one *Chlamydia* peptide by western blotting, total cellular protein is extracted from a sample of blood from an unexposed subject and from a sample of blood from an exposed subject. As a positive control, total cellular protein is also extracted from

Chlamydia cells grown *in vitro*. These protein preparations are then electrophoresed on a sodium dodecyl sulfate-polyacrylamide gel. Thereafter, the proteins are transferred to a membrane (for example, nitrocellulose) by western blotting, and the antibody preparation is incubated with the membrane. After washing the membrane to remove non-specifically bound antibodies, the presence of specifically bound antibodies is detected by the use of an anti-guinea pig antibody conjugated to an enzyme such as alkaline phosphatase; application of the substrate 5-bromo-4-chloro-3-indolyl phosphate/nitro blue tetrazolium results in the production of a dense blue compound by immuno-localized alkaline phosphatase. Antibodies which specifically detect the *Chlamydia* protein will, by this technique, be shown to bind to the *Chlamydia*-extracted sample at a particular protein band (which will be localized at a given position on the gel determined by its molecular weight) and to the proteins extracted from the blood of the exposed subject. No significant binding will be detected to proteins from the unexposed subject.

**EXAMPLE 4: Use of Infection-Specific Sequences
and their Corresponding Peptides and
Antibodies in Diagnostic Assays**

Another aspect of the present invention is a method for detecting the presence of anti-*Chlamydia* antibodies that react with infection-specific *Chlamydia* proteins, *Chlamydia* peptides and *Chlamydia* nucleic acid sequences in biological samples. These methods include detection of antigen and antibody by ELISA and similar techniques, the detection of proteins in a tissue sample by immunofluorescence and related techniques and the detection of specific DNA sequences by specific hybridization and amplification.

One aspect of the invention is an ELISA that detects anti-*Chlamydia* antibodies in a medical specimen. An immunostimulatory infection-specific *Chlamydia* peptide of the present invention is employed as an antigen and is preferably bound to a solid matrix such as a crosslinked dextran such as SEPHADEX (Pharmacia, Piscataway, NJ), agarose, polystyrene, or the wells of a microtiter plate. The polypeptide is admixed with the specimen, such as blood, and the admixture is incubated for a sufficient time to allow antibodies present in the sample to immunoreact with the polypeptide. The presence of the positive immunoreaction is then determined using an ELISA assay, usually involving the use of an enzyme linked to an anti-immunoglobulin that catalyzes the conversion of a chromogenic substrate.

In one embodiment, the solid support to which the polypeptide is attached is the wall of a microtiter assay plate. After attachment of the polypeptide, any nonspecific binding sites on the microtiter well walls are blocked with a protein such as bovine serum albumin. Excess bovine serum albumin is removed by rinsing and the medical specimen is admixed with the polypeptide in the microtiter wells. After a sufficient incubation time, the microtiter wells are rinsed to remove excess sample and then a solution of a second antibody, capable of detecting human antibodies is added to the wells. This second antibody is typically linked to an enzyme such as peroxidase,

alkaline phosphatase or glucose oxidase. For example, the second antibody may be a peroxidase-labeled goat anti-human antibody. After further incubation, excess amounts of the second antibody are removed by rinsing and a solution containing a substrate for the enzyme label (such as hydrogen peroxide for the peroxidase enzyme) and a color-forming dye precursor, such as

5 o-phenylenediamine is added. The combination of *Chlamydia* peptide (bound to the wall of the well), the human anti-*Chlamydia* antibodies (from the specimen), the enzyme-conjugated anti-human antibody and the color substrate will produce a color that can be read using an instrument that determines optical density, such as a spectrophotometer. These readings can be compared to a negative control such as a sample known to be free of anti-*Chlamydia* antibodies. Positive
10 readings indicate the presence of anti-*Chlamydia* antibodies in the specimen, which in turn indicate a prior exposure of the patient to *Chlamydia*.

In another embodiment, antibodies that specifically recognize a *Chlamydia* peptide encoded by the nucleotide sequences disclosed herein are useful in diagnosing the presence of infection-specific *Chlamydia* antigens in a subject or sample. For example, detection of infection-

15 specific antigens that are present in cells or tissues may be done by immunofluorescence, indirect-immunofluorescence and immunohistochemistry. In immunofluorescence, a fluorescent dye is bound directly to the antibody. In indirect-immunofluorescence, the dye is bound to an anti-immunoglobulin. Specific binding occurs between antigen and bound antibody is detected by virtue of fluorescent emissions from the dye moiety. This technique may be particularly useful,
20 for instance, for detection of *Chlamydia* antigen present on a urogenital mucosal smear.

Chlamydia may be present in urogenital mucosa, and a smear on a glass slide may be fixed and bathed in a solution containing an antibody specific to the infection-specific antigen. The slide is then washed to remove the unbound antibody, and a fluorescent anti-immunoglobulin antibody is added. The slide is washed again, and viewed microscopically under an appropriate wavelength of light to detect fluorescence. Fluorescence indicates the presence of *Chlamydia* antigen.
25

Alternatively, a urogenital mucosal smear may be taken, the sample cultured with HeLa cells to produce large amounts of the RB form, and immunofluorescence may then be used to detect infection-specific *Chlamydia* antibodies.

Another aspect of the invention includes the use of nucleic acid primers to detect the presence of *Chlamydia* nucleic acids that encode infection-specific antigens in body samples and thus to diagnose infection. In other embodiments, these oligonucleotide primers will comprise at least 15 contiguous nucleotides of a DNA sequence as shown in SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, or 17. In other embodiments, such oligonucleotides may comprise at least 20 or at least 25 or more contiguous nucleotides of the aforementioned sequences.
30

35 One skilled in the art will appreciate that PCR primers are not required to exactly match the target gene sequence to which they anneal. Therefore, in another embodiment, the oligonucleotides will comprise a sequence of at least 15 nucleotides and preferably at least 20 nucleotides, the oligonucleotide sequence being substantially similar to a DNA sequence set forth

in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, and 17. Such oligonucleotides may share at least about 75%, 85%, 90% or greater sequence identity.

The detection of specific nucleic acid sequences in a sample by polymerase chain reaction amplification (PCR) is discussed in detail in Innis et al., (1990). *PCR Protocols: A Guide to*

5 *Methods and Applications*, Academic Press: San Diego, part 4 in particular. To detect *Chlamydia* sequences, primers based on the sequences disclosed herein would be synthesized, such that PCR amplification of a sample containing *Chlamydia* DNA would result in an amplified fragment of a predicted size. If necessary, the presence of this fragment following amplification of the sample nucleic acid could be detected by dot blot analysis. PCR amplification employing primers based 10 on the sequences disclosed herein may also be employed to quantify the amounts of *Chlamydia* nucleic acid present in a particular sample (see chapters 8 and 9 of Innis et al., (1990)).

Alternatively, probes based on the nucleic acid sequences described herein may be labeled with suitable labels (such a P³² or biotin) and used in hybridization assays to detect the presence of *Chlamydia* nucleic acid in provided samples.

15 Reverse-transcription PCR using these primers may also be utilized to detect the presence of *Chlamydia* RNA which is indicative of an ongoing infection.

EXAMPLE 5: Production of Chlamydia Vaccines

The purified peptides of the present invention may be used directly as immunogens for 20 vaccination. Methods for using purified peptides as vaccines are well known in the art and are described in Yang et al. (1991), Andersen (1994) and Jardim et al. (1990). As is well known in the art, adjuvants such as alum, Complete Freund's Adjuvant (CFA) and Incomplete Freund's Adjuvant (IFA) may be used in formulations of purified peptides as vaccines. Accordingly, one embodiment of the present invention is a vaccine comprising one or more immunostimulatory *C. trachomatis* or *C. psittaci* peptides encoded by nucleotide sequences as shown in the attached 25 sequence listing, together with a pharmaceutically acceptable adjuvant.

Additionally a vaccine may comprise a defined fraction of the disclosed peptide of *C. trachomatis* or *C. psittaci* or may comprise a peptide wherein the gene coding for the peptide shows substantial similarity to the DNA sequences disclosed herein, such as for orthologous genes 30 of *C. pneumoniae* or *C. pecorum*.

Additionally, the vaccines may be formulated using a peptide according to the present invention together with a pharmaceutically acceptable excipient such as water, saline, dextrose and glycerol. The vaccines may also include auxiliary substances such as emulsifying agents and pH buffers.

35 It will be appreciated by one of skill in the art that vaccines formulated as described above may be administered in a number of ways including subcutaneous, intra-muscular and intra-venous injection. Doses of the vaccine administered will vary depending on the antigenicity of the particular peptide or peptide combination employed in the vaccine, and characteristics of the

animal or human patient to be vaccinated. While the determination of individual doses will be within the skill of the administering physician, it is anticipated that doses of between 1 microgram and 1 milligram will be employed.

As with many vaccines, the vaccines of the present invention may routinely be
5 administered several times over the course of a number of weeks to ensure that an effective immune response is triggered. Where such multiple doses are administered, they will normally be administered at from two to twelve week intervals, more usually from three to five week intervals. Periodic boosters at intervals of 1-5 years, usually three years, may be desirable to maintain the desired levels of protective immunity.
10 Alternatively, multiple immunostimulatory peptides may also be administered by expressing the nucleic acids encoding the peptides in a nonpathogenic microorganism, and using this transformed nonpathogenic microorganism as a vaccine.

Finally, a recent development in the field of vaccines is the direct injection of nucleic acid molecules encoding peptide antigens, as described in Janeway & Travers, (1997). Thus, plasmids
15 which include nucleic acid molecules described herein, or which include nucleic acid sequences encoding peptides according to the present invention may be utilized in such DNA vaccination methods.

The vaccine of the invention may be used to inoculate potential animal targets of any of the chlamydial diseases including those caused by *C. trachomatis*, *C. psittaci*, *C. pneumoniae* or
20 *C. pecorum*. Indeed the vaccine of the invention may be used to inoculate animals against any disease that shows immunological cross-protection as a result of exposure to infection-specific *Chlamydia* antigen. The protein or polypeptide is present in the vaccine in an amount sufficient to induce a protective immune response whether through humoral or cell mediated pathways or through both. Such a response protects the immunized animal against chlamydial infections specifically by raising an immune response against the Reticulate Body form of *Chlamydia*.

The above embodiments are set out only by way of example and are not intended to be exclusive, one skilled in the art will understand that the invention may be practiced in various additional ways without departing from the subject of the spirit of the invention.

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CLAIMS

What is claimed is:

1. A purified infection-specific protein comprising an amino acid sequence selected from the group consisting of:
 - 5 (a) SEQ ID NO: 2,
 - (b) SEQ ID NO: 4,
 - (c) SEQ ID NO: 6,
 - (d) SEQ ID NO: 10,
 - (e) SEQ ID NO: 12,
 - 10 (f) an amino acid sequence that differs from an amino acid sequence of (a) to (e) inclusive, by one or more conservative amino acid substitutions, and
(g) an amino acid sequence having at least 60% sequence identity to an amino acid sequence of (a) to (e) inclusive.
2. An isolated nucleic acid molecule encoding a protein according to claim 1.
- 15 3. An isolated nucleic acid molecule according to claim 2 wherein the nucleic acid molecule comprises a nucleic acid sequence selected from the group consisting of:
 - (a) SEQ ID NO: 1,
 - (b) SEQ ID NO: 3,
 - (c) SEQ ID NO: 5,
 - 20 (d) SEQ ID NO: 9, and
 - (e) SEQ ID NO: 11.
4. A recombinant nucleic acid molecule comprising a promoter sequence operably linked to a nucleotide molecule according to claim 2.
5. A vaccine preparation comprising at least one purified peptide comprising at least 25 5 contiguous amino acids selected from the group consisting of:
 - (a) SEQ ID NO: 2,
 - (b) SEQ ID NO: 4,
 - (c) SEQ ID NO: 6,
 - (d) SEQ ID NO: 8,
 - 30 (e) SEQ ID NO: 10,
 - (f) SEQ ID NO: 12,
 - (g) SEQ ID NO: 14,
 - (h) SEQ ID NO: 16, and
 - (i) SEQ ID NO: 18.
- 35 6. The vaccine preparation of claim 5 wherein the peptide comprises at least 10 contiguous amino acids of at least one of the specified sequences.
7. The vaccine preparation of claim 5 wherein the peptide comprises at least 15 contiguous amino acids of at least one of the specified sequences.

8. The vaccine preparation of claim 5 wherein the purified peptide comprises at least 20 contiguous amino acids of at least one of the specified sequences.

9. A vaccine preparation comprising an amino acid sequence selected from the group consisting of:

(a) SEQ ID NO: 2,

(b) SEQ ID NO: 4,

(c) SEQ ID NO: 6,

(d) SEQ ID NO: 8,

10 (e) SEQ ID NO: 10,

(f) SEQ ID NO: 12,

(g) SEQ ID NO: 14,

(h) SEQ ID NO: 16,

(i) SEQ ID NO: 18,

15 (j) an amino acid sequence that differs from an amino acid sequence of (a) to (i) inclusive, by one or more conservative amino acid substitutions, and

(k) an amino acid sequence having at least 60% sequence identity to an amino acid sequence of (a) to (i) inclusive.

10. A method of making a vaccine comprising combining a pharmaceutically acceptable excipient with a purified peptide having an amino acid sequence selected from the group consisting of:

(a) SEQ ID NO: 2,

(b) SEQ ID NO: 4,

(c) SEQ ID NO: 6,

25 (d) SEQ ID NO: 8,

(e) SEQ ID NO: 10,

(f) SEQ ID NO: 12,

(g) SEQ ID NO: 14,

(h) SEQ ID NO: 16,

30 (i) SEQ ID NO: 18,

(j) an amino acid sequence that differs from an amino acid sequence of (a) to (i) inclusive, by one or more conservative amino acid substitutions,

(k) an amino acid sequence having at least 60% sequence identity to an amino acid sequence of (a) to (i) inclusive, and

35 (l) at least 10 contiguous amino acids from an amino acid sequence of (a) to (i) inclusive.

11. A method of vaccination, comprising administering a vaccine preparation according to claim 5 to a mammal.

12. A method of vaccination, comprising administering a vaccine preparation according to claim 9 to a mammal.

13. A method of detecting an infection-specific *Chlamydia* protein in a biological sample comprising: contacting the biological sample with at least one anti-*Chlamydia* antibody, 5 which antibody is an infection-specific antibody, such that a reaction between the antibody and the infection-specific *Chlamydia* protein gives rise to a detectable effect, and detecting the detectable effect.

14. The method of claim 13 wherein the anti-*Chlamydia* antibody binds specifically to a peptide having an amino acid sequence selected from the group consisting of:

10 (a) SEQ ID NO: 2,

(b) SEQ ID NO: 4,

(c) SEQ ID NO: 6,

(d) SEQ ID NO: 8,

(e) SEQ ID NO: 10,

15 (f) SEQ ID NO: 12,

(g) SEQ ID NO: 14,

(h) SEQ ID NO: 16, and

(i) SEQ ID NO: 18.

15. A method of detecting an infection-specific anti-*Chlamydia* antibody in a 20 biological sample comprising: contacting the biological sample with at least one *Chlamydia* peptide, which peptide is an infection specific peptide, such that a reaction between the peptide and the infection-specific anti-*Chlamydia* antibody gives rise to a detectable effect, and detecting the detectable effect.

16. The method of claim 15 wherein the *Chlamydia* peptide comprises at least 5 25 contiguous amino acids of a sequence selected from the group consisting of:

(a) SEQ ID NO: 2,

(b) SEQ ID NO: 4,

(c) SEQ ID NO: 6,

(d) SEQ ID NO: 8,

30 (e) SEQ ID NO: 10,

(f) SEQ ID NO: 12,

(g) SEQ ID NO: 14,

(h) SEQ ID NO: 16, and

(i) SEQ ID NO: 18.

35 17. The method of claim 15 wherein said *Chlamydia* peptide comprises an amino acid sequence selected from the group consisting of:

(a) SEQ ID NO: 2,

(b) SEQ ID NO: 4,

- (c) SEQ ID NO: 6,
- (d) SEQ ID NO: 8,
- (e) SEQ ID NO: 10,
- (f) SEQ ID NO: 12,
- (g) SEQ ID NO: 14,
- (h) SEQ ID NO: 16, and
- (i) SEQ ID NO: 18.

18. A method of treating a *Chlamydial* infection comprising directing a therapeutic agent against a specific target, said target chosen from the group consisting of: (i) an infection-specific protein of *Chlamydia*, (ii) a gene that encodes an infection-specific protein of *Chlamydia* and (iii) an RNA transcript that encodes an infection-specific protein of *Chlamydia*, wherein said therapeutic agent interacts with said target to affect a reduction in pathology.

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100	105	110	
aac caa agt aat ttc aag cgc atg caa aag att atg gaa gaa gtg aaa			384
Asn Gln Ser Asn Phe Lys Arg Met Gln Lys Ile Met Glu Glu Val Lys			
115	120	125	

aaa gct tct gaa act gtg cgt att caa gaa ggc ttg tca gtc ctt ctt	432		
Lys Ala Ser Glu Thr Val Arg Ile Gln Glu Gly Leu Ser Val Leu Leu			
130	135	140	

aac gaa gat att gtc tta tct atc gat agt tcg gca gat aaa acc gat	480		
Asn Glu Asp Ile Val Leu Ser Ile Asp Ser Ser Ala Asp Lys Thr Asp			
145	150	155	160

gct gtt att aaa gtt ctt gat gtt ctt ttc aaa ata att aac atg cga	528		
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agc tag	534
Ser	

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20	25	30	
Arg Cys Leu Glu Glu Ser Ala Leu Gly Lys Lys Glu Ser Ala Glu Phe			
35	40	45	
Glu Lys Met Lys Asn Gln Phe Ser Asn Ser Met Gly Lys Met Glu Glu			
50	55	60	
Glu Leu Ser Ser Ile Tyr Ser Lys Leu Gln Asp Asp Asp Tyr Met Glu			
65	70	75	80
Gly Leu Ser Glu Thr Ala Ala Glu Leu Arg Lys Lys Phe Glu Asp			
85	90	95	
Leu Ser Ala Glu Tyr Asn Thr Ala Gln Gly Gln Tyr Tyr Gln Ile Leu			
100	105	110	
Asn Gln Ser Asn Phe Lys Arg Met Gln Lys Ile Met Glu Glu Val Lys			
115	120	125	
Lys Ala Ser Glu Thr Val Arg Ile Gln Glu Gly Leu Ser Val Leu Leu			
130	135	140	
Asn Glu Asp Ile Val Leu Ser Ile Asp Ser Ser Ala Asp Lys Thr Asp			
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165	170	175	

Ser

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1 5 10 15
gtc aag aat att gtt ctg att gat gga gcg att gat cct cat tca tat 96
Val Lys Asn Ile Val Leu Ile Asp Gly Ala Ile Asp Pro His Ser Tyr
20 25 30
gag atg gtg aag ggg gat gaa gac cga atg gct atg agc cag ctg att 144
Glu Met Val Lys Gly Asp Glu Asp Arg Met Ala Met Ser Gln Leu Ile
35 40 45
ttt tgc aat ggt tta ggt tta gag cat tca gct agt tta cgt aaa cat 192
Phe Cys Asn Gly Leu Gly Leu Glu His Ser Ala Ser Leu Arg Lys His
50 55 60
cta gag ggt aac cca aaa gtc gtt gat tta ggt caa cgt ttg ctt aac 240
Leu Glu Gly Asn Pro Lys Val Val Asp Leu Gly Lys Arg Leu Leu Asn
65 70 75 80
aaa aac tgt ttt gat ctt ctg agt gaa gaa gga ttc cct gac cca cat 288
Lys Asn Cys Phe Asp Leu Leu Ser Glu Glu Gly Phe Pro Asp Pro His
85 90 95
att tgg acg gat atg aga gta tgg ggt gct gat gta aaa gag atg gct 336
Ile Trp Thr Asp Met Arg Val Trp Gly Ala Ala Val Lys Glu Met Ala
100 105 110
gcg gca tta att caa caa ttt cct caa tat gaa gaa gat ttt caa aag 384
Ala Ala Leu Ile Gln Gln Phe Pro Gln Tyr Glu Glu Asp Phe Gln Lys
115 120 125
aat gcg gat cag atc tta tca gag atg gag gaa ctt gat cgt tgg gca 432
Asn Ala Asp Gln Ile Leu Ser Glu Met Glu Glu Leu Asp Arg Trp Ala
130 135 140
gtg cgt tct ctc tct acg att cct gaa aaa aat cgc tat tta gtc aca 480
Val Arg Ser Leu Ser Thr Ile Pro Glu Lys Asn Arg Tyr Leu Val Thr
145 150 155 160
ggc cac aat gcg ttc agt tac ttt act cgt cgg tat cta tcc tct gat 528
Gly His Asn Ala Phe Ser Tyr Phe Thr Arg Arg Tyr Leu Ser Ser Asp
165 170 175
gcg gag aga gtg tct ggg gaa tgg aga tcg cgt tgc att tct cca gaa 576
Ala Glu Arg Val Ser Gly Glu Trp Arg Ser Arg Cys Ile Ser Pro Glu
180 185 190

ggg ttg tct cct gag gct cag att agt atc cga gat att atg cgt gta 624
 Gly Leu Ser Pro Glu Ala Gln Ile Ser Ile Arg Asp Ile Met Arg Val
 195 200 205

gtg gag tat atc tct gca aac gat gta gaa gtt gtc ttt tta gag gat 672
 Val Glu Tyr Ile Ser Ala Asn Asp Val Glu Val Val Phe Leu Glu Asp
 210 215 220

acg tta aat caa gat gct ttg aga aag att gtt tct tgc tct aag agc 720
 Thr Leu Asn Gln Asp Ala Leu Arg Lys Ile Val Ser Cys Ser Lys Ser
 225 230 235 240

gga caa aag att cgt ctc gct aag tct cct tta tat agc gat aat gtc 768
 Gly Gln Lys Ile Arg Leu Ala Lys Ser Pro Leu Tyr Ser Asp Asn Val
 245 250 255

tgt gat aac tat ttt agc acg ttc cag cac aat gtt cgc aca att aca 816
 Cys Asp Asn Tyr Phe Ser Thr Phe Gln His Asn Val Arg Thr Ile Thr
 260 265 270

gaa gaa ttg gga ggg act gtt ctt gaa tag 846
 Glu Glu Leu Gly Gly Thr Val Leu Glu
 275 280

<210> 4

<211> 281

<212> PRT

<213> Chlamydia trachomatis

<400> 4

Met Asn Arg Met Ile Cys Asp Cys Val Ser Arg Ile Thr Gly Asp Arg
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Val Lys Asn Ile Val Leu Ile Asp Gly Ala Ile Asp Pro His Ser Tyr
 20 25 30

Glu Met Val Lys Gly Asp Glu Asp Arg Met Ala Met Ser Gln Leu Ile
 35 40 45

Phe Cys Asn Gly Leu Gly Leu Glu His Ser Ala Ser Leu Arg Lys His
 50 55 60

Leu Glu Gly Asn Pro Lys Val Val Asp Leu Gly Gln Arg Leu Leu Asn
 65 70 75 80

Lys Asn Cys Phe Asp Leu Leu Ser Glu Glu Gly Phe Pro Asp Pro His
 85 90 95

Ile Trp Thr Asp Met Arg Val Trp Gly Ala Ala Val Lys Glu Met Ala
 100 105 110

Ala Ala Leu Ile Gln Gln Phe Pro Gln Tyr Glu Glu Asp Phe Gln Lys
 115 120 125

Asn Ala Asp Gln Ile Leu Ser Glu Met Glu Glu Leu Asp Arg Trp Ala
 130 135 140

Val Arg Ser Leu Ser Thr Ile Pro Glu Lys Asn Arg Tyr Leu Val Thr
 145 150 155 160

Gly His Asn Ala Phe Ser Tyr Phe Thr Arg Arg Tyr Leu Ser Ser Asp
 165 170 175

Ala Glu Arg Val Ser Gly Glu Trp Arg Ser Arg Cys Ile Ser Pro Glu
 180 185 190

Gly Leu Ser Pro Glu Ala Gln Ile Ser Ile Arg Asp Ile Met Arg Val
 195 200 205

Val Glu Tyr Ile Ser Ala Asn Asp Val Glu Val Val Phe Leu Glu Asp
 210 215 220

Thr Leu Asn Gln Asp Ala Leu Arg Lys Ile Val Ser Cys Ser Lys Ser
 225 230 235 240

Gly Gln Lys Ile Arg Leu Ala Lys Ser Pro Leu Tyr Ser Asp Asn Val
 245 250 255

Cys Asp Asn Tyr Phe Ser Thr Phe Gln His Asn Val Arg Thr Ile Thr
 260 265 270

Glu Glu Leu Gly Gly Thr Val Leu Glu
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<210> 5

<211> 861

<212> DNA

<213> Chlamydia trachomatis

<220>

<221> CDS

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1	5	10
		15

tta cag aag aat tgg gag gga ctg ttc ttg aat aga gat aat	gca att	96
Leu Gln Lys Asn Trp Glu Gly Leu Phe Leu Asn Arg Asp Asn Ala Ile		
20	25	30

gct tgg tcc gta gag gat ctt tgt gtt aat tat gat cac tca gac	gtc	144
Ala Trp Ser Val Glu Asp Leu Cys Val Asn Tyr Asp His Ser Asp Val		
35	40	45

tta tgt cac att act ttt tct ctg cct gca ggg gca atg	gtc	192
Leu Cys His Ile Thr Phe Ser Leu Pro Ala Gly Ala Met Ala Ala Ile		
50	55	60

att ggg ccg aat gga gct ggt aaa agt act ttg ctt aag gct	tct tta	240
Ile Gly Pro Asn Gly Ala Gly Lys Ser Thr Leu Leu Lys Ala Ser Leu		
65	70	75
		80

gga ctg att cgt gct tct tct ggc caa agc ttg ttc ttt ggt	cag aga	288
Gly Leu Ile Arg Ala Ser Ser Gly Gln Ser Leu Phe Phe Gly Gln Arg		
85	90	95

ttt tcc aag gca cat cat aga ata gcc tat atg cct caa aga gcg	agt	336
Phe Ser Lys Ala His His Arg Ile Ala Tyr Met Pro Gln Arg Ala Ser		

100	105	110	
gtg gat tgg gat ttc cca atg act gtt ctt gat ctc gtg ttg atg ggg Val Asp Trp Asp Phe Pro Met Thr Val Leu Asp Leu Val Leu Met Gly			384
115	120	125	
tgt tac ggc tat aaa gga ata tgg aat cgt att tcc act gat gat cgt Cys Tyr Gly Tyr Lys Gly Ile Trp Asn Arg Ile Ser Thr Asp Asp Arg			432
130	135	140	
cag gag gct atg cgt att tta gag cgg gtt ggt ttg gaa gct ttt gca Gln Glu Ala Met Arg Ile Leu Glu Arg Val Gly Leu Glu Ala Phe Ala			480
145	150	155	160
aat cgt caa ata ggt aag ctc tct gga gga caa caa cag aga gct ttt Asn Arg Gln Ile Gly Lys Leu Ser Gly Gly Gln Gln Arg Ala Phe			528
165	170	175	
tta gcg cgg tca tta atg caa aaa gca gat ttg tat ctc atg gat gag Leu Ala Arg Ser Leu Met Gln Lys Ala Asp Leu Tyr Leu Met Asp Glu			576
180	185	190	
ctg ttc tct gcg atc gat atg gcc tct tat cag atg gtt gta gat gtt Leu Phe Ser Ala Ile Asp Met Ala Ser Tyr Gln Met Val Val Asp Val			624
195	200	205	
ttg caa gag ctt aaa agc gaa ggg aag act att gtg gtc att cat cat Leu Gln Glu Leu Lys Ser Glu Gly Lys Thr Ile Val Val Ile His His			672
210	215	220	
gat ttg agt aat gtc cgg aag ctt ttt gat cat gtg att tta tta aat Asp Leu Ser Asn Val Arg Lys Leu Phe Asp His Val Ile Leu Leu Asn			720
225	230	235	240
aag cat ctt gtg tgc tct gga agc gta gaa gaa tgc ttg act aaa gaa Lys His Leu Val Cys Ser Gly Ser Val Glu Glu Cys Leu Thr Lys Glu			768
245	250	255	
gcc att ttt cag gct tat ggg tgt gac ttg agc ttt tgg att aca cac Ala Ile Phe Gln Ala Tyr Gly Cys Asp Leu Ser Phe Trp Ile Thr His			816
260	265	270	
tca aat tgt cta gag gca agt acc aag gat cgt gct aga tgc tga Ser Asn Cys Leu Glu Ala Ser Thr Lys Asp Arg Ala Arg Cys			861
275	280	285	
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<212> PRT			
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<400> 6			
Met Ser Val Ile Thr Ile Leu Ala Arg Ser Ser Thr Met Phe Ala Gln			
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Leu Gln Lys Asn Trp Glu Gly Leu Phe Leu Asn Arg Asn Ala Ile			
20 25 30			
Ala Trp Ser Val Glu Asp Leu Cys Val Asn Tyr Asp His Ser Asp Val			
35 40 45			

Leu Cys His Ile Thr Phe Ser Leu Pro Ala Gly Ala Met Ala Ala Ile
 50 55 60

Ile Gly Pro Asn Gly Ala Gly Lys Ser Thr Leu Leu Lys Ala Ser Leu
 65 70 75 80

Gly Leu Ile Arg Ala Ser Ser Gly Gln Ser Leu Phe Phe Gly Gln Arg
 85 90 95

Phe Ser Lys Ala His His Arg Ile Ala Tyr Met Pro Gln Arg Ala Ser
 100 105 110

Val Asp Trp Asp Phe Pro Met Thr Val Leu Asp Leu Val Leu Met Gly
 115 120 125

Cys Tyr Gly Tyr Lys Gly Ile Trp Asn Arg Ile Ser Thr Asp Asp Arg
 130 135 140

Gln Glu Ala Met Arg Ile Leu Glu Arg Val Gly Leu Glu Ala Phe Ala
 145 150 155 160

Asn Arg Gln Ile Gly Lys Leu Ser Gly Gly Gln Gln Gln Arg Ala Phe
 165 170 175

Leu Ala Arg Ser Leu Met Gln Lys Ala Asp Leu Tyr Leu Met Asp Glu
 180 185 190

Leu Phe Ser Ala Ile Asp Met Ala Ser Tyr Gln Met Val Val Asp Val
 195 200 205

Leu Gln Glu Leu Lys Ser Glu Gly Lys Thr Ile Val Val Ile His His
 210 215 220

Asp Leu Ser Asn Val Arg Lys Leu Phe Asp His Val Ile Leu Leu Asn
 225 230 235 240

Lys His Leu Val Cys Ser Gly Ser Val Glu Glu Cys Leu Thr Lys Glu
 245 250 255

Ala Ile Phe Gln Ala Tyr Gly Cys Asp Leu Ser Phe Trp Ile Thr His
 260 265 270

Ser Asn Cys Leu Glu Ala Ser Thr Lys Asp Arg Ala Arg Cys
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<210> 7

<211> 1068

<212> DNA

<213> Chlamydia psittaci

<220>

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<222> (1)..(1068)

<400> 7

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Met Thr Val Ser Thr Asp Asn Thr Ser Pro Val Ile Ser Arg Ala Ser	
1 5 10 15	

tca cct act ttt gga gat cat ggt aag gat ttc gac aac aat aaa att	96																																																																																																																										
Ser Pro Thr Phe Gly Asp His Gly Lys Asp Phe Asp Asn Asn Lys Ile																																																																																																																											
20	25		30	ata ccc att tca ata gaa gct cca act tct tca gct gct gct gta ggg	144	Ile Pro Ile Ser Ile Glu Ala Pro Thr Ser Ser Ala Ala Val Gly		35	40		45	gct aaa acg gct atc gag cct gaa gga aga agc cca cta ctt caa agg	192	Ala Lys Thr Ala Ile Glu Pro Glu Gly Arg Ser Pro Leu Leu Gln Arg		50	55		60	att tgc tat ctt gtt aaa att atc gct gcc atc gcc ctc ttt gtt gtt	240	Ile Cys Tyr Leu Val Lys Ile Ile Ala Ala Ile Ala Leu Phe Val Val		65	70		75		80	ggt atc gca gcc tta gtt tgc tta tat ctc ggt agc gtt atc tca acg	288	Gly Ile Ala Ala Leu Val Cys Leu Tyr Leu Gly Ser Val Ile Ser Thr		85	90		95	cct tct ctt att ctt atg ctt gcg atc atg ctt gta tcc ttt gtg atc	336	Pro Ser Leu Ile Leu Met Leu Ala Ile Met Leu Val Ser Phe Val Ile		100	105		110	gtt att acg gca att cga gat ggc aca ccg tct caa gtg gtc cgt cac	384	Val Ile Thr Ala Ile Arg Asp Gly Thr Pro Ser Gln Val Val Arg His		115	120		125	atg aaa cag caa att cag caa ttt ggc gaa gaa aac acg cgt tta cat	432	Met Lys Gln Gln Ile Gln Gln Phe Gly Glu Glu Asn Thr Arg Leu His		130	135		140	acc gca gta gaa aat cta aaa gct gtt aac gtt gag ctc tca gag caa	480	Thr Ala Val Glu Asn Leu Lys Ala Val Asn Val Glu Leu Ser Glu Gln		145	150		155		160	att aac caa ctt aaa caa cta cat act aga tta tcg gat ttt ggt gat	528	Ile Asn Gln Leu Lys Gln Leu His Thr Arg Leu Ser Asp Phe Gly Asp		165	170		175	agg ctt gaa gcg aat acc ggt gat ttt act gca ctt att gcg gat ttc	576	Arg Leu Glu Ala Asn Thr Gly Asp Phe Thr Ala Leu Ile Ala Asp Phe		180	185		190	caa ctc agt ctg gaa gag ttt aag ttc gtc ttg aaa gag acc ttt	624	Gln Leu Ser Ile Glu Glu Phe Lys Ser Val Gly Thr Lys Val Glu Thr		195	200		205	atg ctc tct cca ttt gag aaa tta gct cag tct ttg aaa gag acc ttt	672	Met Leu Ser Pro Phe Glu Lys Leu Ala Gln Ser Leu Lys Glu Thr Phe		210	215		220	tct caa gaa gct ttg cag gca atg atg tcc tct gta act gag tta aga	720	Ser Gln Glu Ala Val Gln Ala Met Met Ser Ser Val Thr Glu Leu Arg		225	230		235		240	acc aat ttg aat gca ttg aaa gag ctt ata aca gag aat aaa acc gta	768	Thr Asn Leu Asn Ala Leu Lys Glu Leu Ile Thr Glu Asn Lys Thr Val		245	250		255	ata gag caa cta aaa gct gat gct caa ctt aga gaa gag caa gtg cgg	816
	30																																																																																																																										
ata ccc att tca ata gaa gct cca act tct tca gct gct gct gta ggg	144																																																																																																																										
Ile Pro Ile Ser Ile Glu Ala Pro Thr Ser Ser Ala Ala Val Gly																																																																																																																											
35	40		45	gct aaa acg gct atc gag cct gaa gga aga agc cca cta ctt caa agg	192	Ala Lys Thr Ala Ile Glu Pro Glu Gly Arg Ser Pro Leu Leu Gln Arg		50	55		60	att tgc tat ctt gtt aaa att atc gct gcc atc gcc ctc ttt gtt gtt	240	Ile Cys Tyr Leu Val Lys Ile Ile Ala Ala Ile Ala Leu Phe Val Val		65	70		75		80	ggt atc gca gcc tta gtt tgc tta tat ctc ggt agc gtt atc tca acg	288	Gly Ile Ala Ala Leu Val Cys Leu Tyr Leu Gly Ser Val Ile Ser Thr		85	90		95	cct tct ctt att ctt atg ctt gcg atc atg ctt gta tcc ttt gtg atc	336	Pro Ser Leu Ile Leu Met Leu Ala Ile Met Leu Val Ser Phe Val Ile		100	105		110	gtt att acg gca att cga gat ggc aca ccg tct caa gtg gtc cgt cac	384	Val Ile Thr Ala Ile Arg Asp Gly Thr Pro Ser Gln Val Val Arg His		115	120		125	atg aaa cag caa att cag caa ttt ggc gaa gaa aac acg cgt tta cat	432	Met Lys Gln Gln Ile Gln Gln Phe Gly Glu Glu Asn Thr Arg Leu His		130	135		140	acc gca gta gaa aat cta aaa gct gtt aac gtt gag ctc tca gag caa	480	Thr Ala Val Glu Asn Leu Lys Ala Val Asn Val Glu Leu Ser Glu Gln		145	150		155		160	att aac caa ctt aaa caa cta cat act aga tta tcg gat ttt ggt gat	528	Ile Asn Gln Leu Lys Gln Leu His Thr Arg Leu Ser Asp Phe Gly Asp		165	170		175	agg ctt gaa gcg aat acc ggt gat ttt act gca ctt att gcg gat ttc	576	Arg Leu Glu Ala Asn Thr Gly Asp Phe Thr Ala Leu Ile Ala Asp Phe		180	185		190	caa ctc agt ctg gaa gag ttt aag ttc gtc ttg aaa gag acc ttt	624	Gln Leu Ser Ile Glu Glu Phe Lys Ser Val Gly Thr Lys Val Glu Thr		195	200		205	atg ctc tct cca ttt gag aaa tta gct cag tct ttg aaa gag acc ttt	672	Met Leu Ser Pro Phe Glu Lys Leu Ala Gln Ser Leu Lys Glu Thr Phe		210	215		220	tct caa gaa gct ttg cag gca atg atg tcc tct gta act gag tta aga	720	Ser Gln Glu Ala Val Gln Ala Met Met Ser Ser Val Thr Glu Leu Arg		225	230		235		240	acc aat ttg aat gca ttg aaa gag ctt ata aca gag aat aaa acc gta	768	Thr Asn Leu Asn Ala Leu Lys Glu Leu Ile Thr Glu Asn Lys Thr Val		245	250		255	ata gag caa cta aaa gct gat gct caa ctt aga gaa gag caa gtg cgg	816								
	45																																																																																																																										
gct aaa acg gct atc gag cct gaa gga aga agc cca cta ctt caa agg	192																																																																																																																										
Ala Lys Thr Ala Ile Glu Pro Glu Gly Arg Ser Pro Leu Leu Gln Arg																																																																																																																											
50	55		60	att tgc tat ctt gtt aaa att atc gct gcc atc gcc ctc ttt gtt gtt	240	Ile Cys Tyr Leu Val Lys Ile Ile Ala Ala Ile Ala Leu Phe Val Val		65	70		75		80	ggt atc gca gcc tta gtt tgc tta tat ctc ggt agc gtt atc tca acg	288	Gly Ile Ala Ala Leu Val Cys Leu Tyr Leu Gly Ser Val Ile Ser Thr		85	90		95	cct tct ctt att ctt atg ctt gcg atc atg ctt gta tcc ttt gtg atc	336	Pro Ser Leu Ile Leu Met Leu Ala Ile Met Leu Val Ser Phe Val Ile		100	105		110	gtt att acg gca att cga gat ggc aca ccg tct caa gtg gtc cgt cac	384	Val Ile Thr Ala Ile Arg Asp Gly Thr Pro Ser Gln Val Val Arg His		115	120		125	atg aaa cag caa att cag caa ttt ggc gaa gaa aac acg cgt tta cat	432	Met Lys Gln Gln Ile Gln Gln Phe Gly Glu Glu Asn Thr Arg Leu His		130	135		140	acc gca gta gaa aat cta aaa gct gtt aac gtt gag ctc tca gag caa	480	Thr Ala Val Glu Asn Leu Lys Ala Val Asn Val Glu Leu Ser Glu Gln		145	150		155		160	att aac caa ctt aaa caa cta cat act aga tta tcg gat ttt ggt gat	528	Ile Asn Gln Leu Lys Gln Leu His Thr Arg Leu Ser Asp Phe Gly Asp		165	170		175	agg ctt gaa gcg aat acc ggt gat ttt act gca ctt att gcg gat ttc	576	Arg Leu Glu Ala Asn Thr Gly Asp Phe Thr Ala Leu Ile Ala Asp Phe		180	185		190	caa ctc agt ctg gaa gag ttt aag ttc gtc ttg aaa gag acc ttt	624	Gln Leu Ser Ile Glu Glu Phe Lys Ser Val Gly Thr Lys Val Glu Thr		195	200		205	atg ctc tct cca ttt gag aaa tta gct cag tct ttg aaa gag acc ttt	672	Met Leu Ser Pro Phe Glu Lys Leu Ala Gln Ser Leu Lys Glu Thr Phe		210	215		220	tct caa gaa gct ttg cag gca atg atg tcc tct gta act gag tta aga	720	Ser Gln Glu Ala Val Gln Ala Met Met Ser Ser Val Thr Glu Leu Arg		225	230		235		240	acc aat ttg aat gca ttg aaa gag ctt ata aca gag aat aaa acc gta	768	Thr Asn Leu Asn Ala Leu Lys Glu Leu Ile Thr Glu Asn Lys Thr Val		245	250		255	ata gag caa cta aaa gct gat gct caa ctt aga gaa gag caa gtg cgg	816																
	60																																																																																																																										
att tgc tat ctt gtt aaa att atc gct gcc atc gcc ctc ttt gtt gtt	240																																																																																																																										
Ile Cys Tyr Leu Val Lys Ile Ile Ala Ala Ile Ala Leu Phe Val Val																																																																																																																											
65	70		75		80	ggt atc gca gcc tta gtt tgc tta tat ctc ggt agc gtt atc tca acg	288	Gly Ile Ala Ala Leu Val Cys Leu Tyr Leu Gly Ser Val Ile Ser Thr		85	90		95	cct tct ctt att ctt atg ctt gcg atc atg ctt gta tcc ttt gtg atc	336	Pro Ser Leu Ile Leu Met Leu Ala Ile Met Leu Val Ser Phe Val Ile		100	105		110	gtt att acg gca att cga gat ggc aca ccg tct caa gtg gtc cgt cac	384	Val Ile Thr Ala Ile Arg Asp Gly Thr Pro Ser Gln Val Val Arg His		115	120		125	atg aaa cag caa att cag caa ttt ggc gaa gaa aac acg cgt tta cat	432	Met Lys Gln Gln Ile Gln Gln Phe Gly Glu Glu Asn Thr Arg Leu His		130	135		140	acc gca gta gaa aat cta aaa gct gtt aac gtt gag ctc tca gag caa	480	Thr Ala Val Glu Asn Leu Lys Ala Val Asn Val Glu Leu Ser Glu Gln		145	150		155		160	att aac caa ctt aaa caa cta cat act aga tta tcg gat ttt ggt gat	528	Ile Asn Gln Leu Lys Gln Leu His Thr Arg Leu Ser Asp Phe Gly Asp		165	170		175	agg ctt gaa gcg aat acc ggt gat ttt act gca ctt att gcg gat ttc	576	Arg Leu Glu Ala Asn Thr Gly Asp Phe Thr Ala Leu Ile Ala Asp Phe		180	185		190	caa ctc agt ctg gaa gag ttt aag ttc gtc ttg aaa gag acc ttt	624	Gln Leu Ser Ile Glu Glu Phe Lys Ser Val Gly Thr Lys Val Glu Thr		195	200		205	atg ctc tct cca ttt gag aaa tta gct cag tct ttg aaa gag acc ttt	672	Met Leu Ser Pro Phe Glu Lys Leu Ala Gln Ser Leu Lys Glu Thr Phe		210	215		220	tct caa gaa gct ttg cag gca atg atg tcc tct gta act gag tta aga	720	Ser Gln Glu Ala Val Gln Ala Met Met Ser Ser Val Thr Glu Leu Arg		225	230		235		240	acc aat ttg aat gca ttg aaa gag ctt ata aca gag aat aaa acc gta	768	Thr Asn Leu Asn Ala Leu Lys Glu Leu Ile Thr Glu Asn Lys Thr Val		245	250		255	ata gag caa cta aaa gct gat gct caa ctt aga gaa gag caa gtg cgg	816																								
	75		80	ggt atc gca gcc tta gtt tgc tta tat ctc ggt agc gtt atc tca acg	288	Gly Ile Ala Ala Leu Val Cys Leu Tyr Leu Gly Ser Val Ile Ser Thr		85	90		95	cct tct ctt att ctt atg ctt gcg atc atg ctt gta tcc ttt gtg atc	336	Pro Ser Leu Ile Leu Met Leu Ala Ile Met Leu Val Ser Phe Val Ile		100	105		110	gtt att acg gca att cga gat ggc aca ccg tct caa gtg gtc cgt cac	384	Val Ile Thr Ala Ile Arg Asp Gly Thr Pro Ser Gln Val Val Arg His		115	120		125	atg aaa cag caa att cag caa ttt ggc gaa gaa aac acg cgt tta cat	432	Met Lys Gln Gln Ile Gln Gln Phe Gly Glu Glu Asn Thr Arg Leu His		130	135		140	acc gca gta gaa aat cta aaa gct gtt aac gtt gag ctc tca gag caa	480	Thr Ala Val Glu Asn Leu Lys Ala Val Asn Val Glu Leu Ser Glu Gln		145	150		155		160	att aac caa ctt aaa caa cta cat act aga tta tcg gat ttt ggt gat	528	Ile Asn Gln Leu Lys Gln Leu His Thr Arg Leu Ser Asp Phe Gly Asp		165	170		175	agg ctt gaa gcg aat acc ggt gat ttt act gca ctt att gcg gat ttc	576	Arg Leu Glu Ala Asn Thr Gly Asp Phe Thr Ala Leu Ile Ala Asp Phe		180	185		190	caa ctc agt ctg gaa gag ttt aag ttc gtc ttg aaa gag acc ttt	624	Gln Leu Ser Ile Glu Glu Phe Lys Ser Val Gly Thr Lys Val Glu Thr		195	200		205	atg ctc tct cca ttt gag aaa tta gct cag tct ttg aaa gag acc ttt	672	Met Leu Ser Pro Phe Glu Lys Leu Ala Gln Ser Leu Lys Glu Thr Phe		210	215		220	tct caa gaa gct ttg cag gca atg atg tcc tct gta act gag tta aga	720	Ser Gln Glu Ala Val Gln Ala Met Met Ser Ser Val Thr Glu Leu Arg		225	230		235		240	acc aat ttg aat gca ttg aaa gag ctt ata aca gag aat aaa acc gta	768	Thr Asn Leu Asn Ala Leu Lys Glu Leu Ile Thr Glu Asn Lys Thr Val		245	250		255	ata gag caa cta aaa gct gat gct caa ctt aga gaa gag caa gtg cgg	816																										
	80																																																																																																																										
ggt atc gca gcc tta gtt tgc tta tat ctc ggt agc gtt atc tca acg	288																																																																																																																										
Gly Ile Ala Ala Leu Val Cys Leu Tyr Leu Gly Ser Val Ile Ser Thr																																																																																																																											
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	95																																																																																																																										
cct tct ctt att ctt atg ctt gcg atc atg ctt gta tcc ttt gtg atc	336																																																																																																																										
Pro Ser Leu Ile Leu Met Leu Ala Ile Met Leu Val Ser Phe Val Ile																																																																																																																											
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Arg Leu Glu Ala Asn Thr Gly Asp Phe Thr Ala Leu Ile Ala Asp Phe																																																																																																																											
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ata gag caa cta aaa gct gat gct caa ctt aga gaa gag caa gtg cgg	816																																																																																																																										

Ile	Glu	Gln	Leu	Lys	Ala	Asp	Ala	Gln	Leu	Arg	Glu	Glu	Gln	Val	Arg
260									265					270	

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Phe	Leu	Glu	Lys	Arg	Lys	Gln	Glu	Leu	Glu	Glu	Ala	Cys	Ser	Thr	Leu	
275								280				285				

tcc	cat	tca	att	ggc	act	cta	gca	tcc	aca	acc	ctt	cta	aag	gac	912	
Ser	His	Ser	Ile	Ala	Thr	Leu	Gln	Glu	Ser	Thr	Thr	Leu	Leu	Lys	Asp	
290					295							300				

tct	aca	act	aac	tta	cat	gca	gtt	gaa	agt	cgt	ctt	atc	ggg	gtt	atg	960
Ser	Thr	Thr	Asn	Leu	His	Ala	Val	Glu	Ser	Arg	Leu	Ile	Gly	Val	Met	
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Val	Gln	Asp	Gly	Ala	Glu	Ser	Ser	Thr	Val	Glu	Glu	Ala	Ser	Gln	Asp	
325									330					335		

gat	agc	gcg	caa	ccc	caa	gat	gaa	aat	caa	tct	gat	gct	gga	gag	cat	1056
Asp	Ser	Ala	Gln	Pro	Gln	Asp	Glu	Asn	Gln	Ser	Asp	Ala	Gly	Glu	His	
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aaa	gat	agt	taa												1068
Lys	Asp	Ser													
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Ile	Pro	Ile	Ser	Ile	Glu	Ala	Pro	Thr	Ser	Ser	Ala	Ala	Ala	Val	Gly	
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Ala	Lys	Thr	Ala	Ile	Glu	Pro	Glu	Gly	Arg	Ser	Pro	Leu	Leu	Gln	Arg	
50								55					60			

Ile	Cys	Tyr	Leu	Val	Lys	Ile	Ile	Ala	Ala	Ile	Ala	Leu	Phe	Val	Val	
65					70					75			80			

Gly	Ile	Ala	Ala	Leu	Val	Cys	Leu	Tyr	Leu	Gly	Ser	Val	Ile	Ser	Thr	
85								90					95			

Pro	Ser	Leu	Ile	Leu	Met	Leu	Ala	Ile	Met	Leu	Val	Ser	Phe	Val	Ile	
100								105					110			

Val	Ile	Thr	Ala	Ile	Arg	Asp	Gly	Thr	Pro	Ser	Gln	Val	Val	Arg	His	
115								120					125			

Met	Lys	Gln	Gln	Ile	Gln	Gln	Phe	Gly	Glu	Glu	Asn	Thr	Arg	Leu	His	
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 145 150 155 160
 Ile Asn Gln Leu Lys Gln Leu His Thr Arg Leu Ser Asp Phe Gly Asp
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 Arg Leu Glu Ala Asn Thr Gly Asp Phe Thr Ala Leu Ile Ala Asp Phe
 180 185 190
 Gln Leu Ser Leu Glu Glu Phe Lys Ser Val Gly Thr Lys Val Glu Thr
 195 200 205
 Met Leu Ser Pro Phe Glu Lys Leu Ala Gln Ser Leu Lys Glu Thr Phe
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 Ser Gln Glu Ala Val Gln Ala Met Met Ser Ser Val Thr Glu Leu Arg
 225 230 235 240
 Thr Asn Leu Asn Ala Leu Lys Glu Leu Ile Thr Glu Asn Lys Thr Val
 245 250 255
 Ile Glu Gln Leu Lys Ala Asp Ala Gln Leu Arg Glu Glu Gln Val Arg
 260 265 270
 Phe Leu Glu Lys Arg Lys Gln Glu Leu Glu Glu Ala Cys Ser Thr Leu
 275 280 285
 Ser His Ser Ile Ala Thr Leu Gln Glu Ser Thr Thr Leu Leu Lys Asp
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 Asp Val Leu Ile Ala Phe Asn Arg Lys Leu Asn Leu Val Glu Gln Gln
 20 25 30

gca aaa gaa ctt gaa acg aaa gtc agt ttg gta gac aga aca gct act Ala Lys Glu Leu Glu Thr Lys Val Ser Leu Val Asp Arg Thr Ala Thr 35 40 45	144
tta tca ctt acc act ggc aat aat gta gcc acg gat gta ctc ctt tta Leu Ser Leu Thr Thr Gly Asn Asn Val Ala Thr Asp Val Leu Leu 50 55 60	192
aaa gat gag gtt gca gaa cta aaa gga tgt ttg tct gca gtt acg gat Lys Asp Glu Val Ala Glu Leu Lys Gly Cys Leu Ser Ala Val Thr Asp 65 70 75 80	240
cta tta atc cgc tca ggc tca tca aga aca cct ggg ggt gct cct aat Leu Leu Ile Arg Ser Gly Ser Ser Arg Thr Pro Gly Gly Ala Pro Asn 85 90 95	288
cca gaa ggc act aat tac cta ata gga tgc aca cct cct tct ctt tgc Pro Glu Gly Thr Asn Tyr Leu Ile Gly Cys Thr Pro Pro Ser Leu Cys 100 105 110	336
gct aaa ctt aca gcg tta gcg tta aca att ata gcc ctc att gct atc Ala Lys Leu Thr Ala Leu Ala Leu Thr Ile Ile Ala Leu Ile Ala Ile 115 120 125	384
aca gta ctt gtt atc tgt att gtt act gtt tgc ggc ggt ttc ccc cta Thr Val Leu Val Ile Cys Ile Val Thr Val Cys Gly Gly Phe Pro Leu 130 135 140	432
ttt att tcc cta ctc aac atg tac aca gtt ggt gct tgt ata tcc tta Phe Ile Ser Leu Leu Asn Met Tyr Thr Val Gly Ala Cys Ile Ser Leu 145 150 155 160	480
ccg atc att tcg tgt gcc gca gtt tca atg atg att cta tgc tca cat Pro Ile Ile Ser Cys Ala Ala Val Ser Met Met Ile Leu Cys Ser His 165 170 175	528
tct att aac tct tta tta aga aac agg cct gcg atc tat atg act aac Ser Ile Asn Ser Leu Leu Arg Asn Arg Pro Ala Ile Tyr Met Thr Asn 180 185 190	576
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Asp Val Leu Ile Ala Phe Asn Arg Lys Leu Asn Leu Val Glu Gln Gln 20 25 30
Ala Lys Glu Leu Glu Thr Lys Val Ser Leu Val Asp Arg Thr Ala Thr 35 40 45
Leu Ser Leu Thr Thr Gly Asn Asn Val Ala Thr Asp Val Leu Leu Leu

50	55	60	
Lys Asp Glu Val Ala Glu Leu Lys	Gly Cys Leu Ser Ala Val Thr Asp		
65	70	75	80
Leu Leu Ile Arg Ser Gly Ser Ser Arg Thr Pro Gly Gly Ala Pro Asn			
85	90	95	
Pro Glu Gly Thr Asn Tyr Leu Ile Gly Cys Thr Pro Pro Ser Leu Cys			
100	105	110	
Ala Lys Leu Thr Ala Leu Ala Leu Thr Ile Ile Ala Leu Ile Ala Ile			
115	120	125	
Thr Val Leu Val Ile Cys Ile Val Thr Val Cys Gly Gly Phe Pro Leu			
130	135	140	
Phe Ile Ser Leu Leu Asn Met Tyr Thr Val Gly Ala Cys Ile Ser Leu			
145	150	155	160
Pro Ile Ile Ser Cys Ala Ala Val Ser Met Met Ile Leu Cys Ser His			
165	170	175	
Ser Ile Asn Ser Leu Leu Arg Asn Arg Pro Ala Ile Tyr Met Thr Asn			
180	185	190	
Asn Phe Gln Thr Glu Ser			
195			
<210> 11			
<211> 561			
<212> DNA			
<213> Chlamydia psittaci			
<220>			
<221> CDS			
<222> (1)..(561)			
<400> 11			
atg acc tct gta aga acc gat tta act cca ggc gac acc tca ctc caa			48
Met Thr Ser Val Arg Thr Asp Leu Thr Pro Gly Asp Thr Ser Leu Gln			
1	5	10	15
tct tct tta tta aat ccg agt gat ctc aca aca caa cta tcc aac ctc			96
Ser Ser Leu Leu Asn Pro Ser Asp Leu Thr Thr Gln Leu Ser Asn Leu			
20	25	30	
cag act gtt ctc gca ggg ata caa caa caa cat cct tta aac ggt ggt			144
Gln Thr Val Leu Ala Gly Ile Gln Gln Gln His Pro Leu Asn Gly Gly			
35	40	45	
tgg cct cag cat cat cct act ggc gct gca gat caa aat tat ctc atg			192
Trp Pro Gln His His Pro Thr Gly Ala Ala Asp Gln Asn Tyr Leu Met			
50	55	60	
cgt ctg atg caa tct cat atg gca agt acc gta tca gca gta tct gaa			240
Arg Leu Met Gln Ser His Met Ala Ser Thr Val Ser Ala Val Ser Glu			
65	70	75	80
tta aga acc gaa gtc act gca atc aag aca aaa ttg cac ggg cta tct			288

Leu Arg Thr Glu Val Thr Ala Ile Lys Thr Lys Leu His Gly Leu Ser
 85 90 95 336
 act cca gct aat gtt tgc agc ggt cct atg gct cta gcc gct ttt ctt
 Thr Pro Ala Asn Val Cys Ser Gly Pro Met Ala Leu Ala Ala Phe Leu
 100 105 110 115 120 125 384
 cta gct ata tct tta gtt gcg att atc atc att gtt tta gcc tcc tta
 Leu Ala Ile Ser Leu Val Ala Ile Ile Ile Val Leu Ala Ser Leu
 115 120 125 130 135 140 145 155 160 432
 ggc ctt gca ggc ata cta cct caa gct gcc gct atc tta gtg aat aca
 Gly Leu Ala Gly Ile Leu Pro Gln Ala Ala Ala Ile Leu Val Asn Thr
 130 135 140 145 150 155 160 165 170 175 528
 gca aac tct ata tgg gct att gtt agc gct tcg ata gtc act gtt atc
 Ala Asn Ser Ile Trp Ala Ile Val Ser Ala Ser Ile Val Thr Val Ile
 145 150 155 160 165 170 175 180 185 561
 tgc tta att agc gtg cta tgc ata acg cta att cga cac cat aaa ccc
 Cys Leu Ile Ser Val Leu Cys Ile Thr Leu Ile Arg His His Lys Pro
 165 170 175
 tta cct att gaa act agg cct acc gga cat taa
 Leu Pro Ile Glu Thr Arg Pro Thr Gly His
 180 185
 <210> 12
 <211> 186
 <212> PRT
 <213> Chlamydia psittaci
 <400> 12
 Met Thr Ser Val Arg Thr Asp Leu Thr Pro Gly Asp Thr Ser Leu Gln
 1 5 10 15
 Ser Ser Leu Leu Asn Pro Ser Asp Leu Thr Thr Gln Leu Ser Asn Leu
 20 25 30
 Gln Thr Val Leu Ala Gly Ile Gln Gln Gln His Pro Leu Asn Gly Gly
 35 40 45
 Trp Pro Gln His His Pro Thr Gly Ala Ala Asp Gln Asn Tyr Leu Met
 50 55 60
 Arg Leu Met Gln Ser His Met Ala Ser Thr Val Ser Ala Val Ser Glu
 65 70 75 80
 Leu Arg Thr Glu Val Thr Ala Ile Lys Thr Lys Leu His Gly Leu Ser
 85 90 95
 Thr Pro Ala Asn Val Cys Ser Gly Pro Met Ala Leu Ala Ala Phe Leu
 100 105 110
 Leu Ala Ile Ser Leu Val Ala Ile Ile Ile Val Leu Ala Ser Leu
 115 120 125
 Gly Leu Ala Gly Ile Leu Pro Gln Ala Ala Ala Ile Leu Val Asn Thr
 130 135 140

Ala Asn Ser Ile Trp Ala Ile Val Ser Ala Ser Ile Val Thr Val Ile
 145 150 155 160

Cys Leu Ile Ser Val Leu Cys Ile Thr Leu Ile Arg His His Lys Pro
 165 170 175

Leu Pro Ile Glu Thr Arg Pro Thr Gly His
 180 185

<210> 13
<211> 822
<212> DNA
<213> Chlamydia trachomatis

<220>
<221> CDS
<222> (1)..(822)

<400> 13

atg aca acg cct act cta atc gtg att cct cca tct ccc cct gca cct	48
Met Thr Thr Pro Thr Leu Ile Val Ile Pro Pro Ser Pro Pro Ala Pro	
1 5 10 15	

tcc tac tca gcc aat cgc gta cct caa cct tct ttg atg gac aaa att	96
Ser Tyr Ser Ala Asn Arg Val Pro Gln Pro Ser Leu Met Asp Lys Ile	
20 25 30	

aag aaa ata gca gcc att gcc tcc cta att ctt ata ggc aca ata ggc	144
Lys Lys Ile Ala Ala Ile Ala Ser Leu Ile Leu Ile Gly Thr Ile Gly	
35 40 45	

ttt tta gct ctt ttg gga cat ctt gtt ggc ttt ctg atc gct cca caa	192
Phe Leu Ala Leu Leu Gly His Leu Val Gly Phe Leu Ile Ala Pro Gln	
50 55 60	

atc act att gtt ctt ctt gcc cta ttc att acc tca tta gca ggg aat	240
Ile Thr Ile Val Leu Leu Ala Leu Phe Ile Thr Ser Leu Ala Gly Asn	
65 70 75 80	

gct ctt tat cta cag aaa acc gct aat cta cat cta tac cag gat ctg	288
Ala Leu Tyr Leu Gln Lys Thr Ala Asn Leu His Leu Tyr Gln Asp Leu	
85 90 95	

caa aga gaa gtt ggg tct cta aaa gaa att aat ttc atg ctg agc gtt	336
Gln Arg Glu Val Gly Ser Leu Lys Glu Ile Asn Phe Met Leu Ser Val	
100 105 110	

cta cag aaa gaa ttt ctt cat tta tct aaa gaa ttt gca acg aca tct	384
Leu Gln Lys Glu Phe Leu His Leu Ser Lys Glu Phe Ala Thr Ser	
115 120 125	

aaa gac ctc tct gct gta tct caa gat ttt tat tct tgt ttg caa gga	432
Lys Asp Leu Ser Ala Val Ser Gln Asp Phe Tyr Ser Cys Leu Gln Gly	
130 135 140	

ttt aga gat aac tat aaa ggt ttt gaa tct ctt ttg gat gag tat aaa	480
Phe Arg Asp Asn Tyr Lys Gly Phe Glu Ser Leu Leu Asp Glu Tyr Lys	
145 150 155 160	

aac tct aca gaa gaa atg cgc aaa ctc ttt tcg caa gaa atc ata gca	528
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Asn Ser Thr Glu Glu Met Arg Lys Leu Phe Ser Gln Glu Ile Ile Ala
165 170 175

```

gat ctt aaa ggc tct gtt gcc tca tta aga gag gaa atc cga ttc cta 576
Asp Ile Lys Gly Ser Val Ala Ser Leu Arg Glu Glu Ile Arg Phe Leu
          180      185      190

```

```

acc cca tta gca gaa gaa gtt cgc cga tta gcg cat aac cag gaa tca 624
Thr Pro Leu Ala Glu Glu Val Arg Arg Leu Ala His Asn Gln Glu Ser
195 200 205

```

```

tta aca gcg gct att gaa gaa tta aaa aca att cgt gat agc tta cga 672
Leu Thr Ala Ala Ile Glu Glu Leu Lys Thr Ile Arg Asp Ser Leu Arg
   210           215           220

```

```

gat gaa att gga caa ctt tca caa ctt tct aaa act ctt acc agt caa 720
Asp Glu Ile Gly Gln Leu Ser Gln Leu Ser Lys Thr Leu Thr Ser Gln
225      230          235          240

```

```

att gca tta caa cga aaa gag agc tca gat ctg tgt tcc cag ata aga 768
Ile Ala Leu Gln Arg Lys Glu Ser Ser Asp Leu Cys Ser Gln Ile Arg
          245           250           255

```

```

gag acg ctc tcc tcc ccc aga aag tct gca tca ccc tct aca aaa agc 816
Glu Thr Leu Ser Ser Pro Arg Lys Ser Ala Ser Pro Ser Thr Lys Ser
          260      265      270

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tcc tag 822
Ser

<210> 14
<211> 273
<212> PRT
<213> Chlamydia trachomatis

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<400> 14
Met Thr Thr Pro Thr Leu Ile Val Ile Pro Pro Ser Pro Pro Ala Pro
   1           5           10          15

Ser Tyr Ser Ala Asn Arg Val Pro Gln Pro Ser Leu Met Asp Lys Ile
   20          25          30

```

Lys Lys Ile Ala Ala Ile Ala Ser Leu Ile Leu Ile Gly Thr Ile Gly
35 40 45

Phe Leu Ala Leu Leu Gly His Leu Val Gly Phe Leu Ile Ala Pro Gln
50 55 60

Ile Thr Ile Val Leu Leu Ala Leu Phe Ile Thr Ser Leu Ala Gly Asn
65 70 75 80

Ala Leu Tyr Leu Gln Lys Thr Ala Asn Leu His Leu Tyr Gln Asp Leu
85 90 95

Gln Arg Glu Val Gly Ser Leu Lys Glu Ile Asn Phe Met Leu Ser Val
100 105 110

Leu Gln Lys Glu Phe Leu His Leu Ser Lys Glu Phe Ala Thr Thr Ser
115 120 125

Lys Asp Leu Ser Ala Val Ser Gln Asp Phe Tyr Ser Cys Leu Gln Gly
 130 135 140

Phe Arg Asp Asn Tyr Lys Gly Phe Ser Leu Leu Asp Glu Tyr Lys
 145 150 155 160

Asn Ser Thr Glu Glu Met Arg Lys Leu Phe Ser Gln Glu Ile Ile Ala
 165 170 175

Asp Leu Lys Gly Ser Val Ala Ser Leu Arg Glu Glu Ile Arg Phe Leu
 180 185 190

Thr Pro Leu Ala Glu Glu Val Arg Arg Leu Ala His Asn Gln Glu Ser
 195 200 205

Leu Thr Ala Ala Ile Glu Glu Leu Lys Thr Ile Arg Asp Ser Leu Arg
 210 215 220

Asp Glu Ile Gly Gln Leu Ser Gln Leu Ser Lys Thr Leu Thr Ser Gln
 225 230 235 240

Ile Ala Leu Gln Arg Lys Glu Ser Ser Asp Leu Cys Ser Gln Ile Arg
 245 250 255

Glu Thr Leu Ser Ser Pro Arg Lys Ser Ala Ser Pro Ser Thr Lys Ser
 260 265 270

Ser

<210> 15

<211> 348

<212> DNA

<213> Chlamydia trachomatis

<220>

<221> CDS

<222> (1)..(348)

<400> 15

atg gtt cat tct gta tac aat tca ttg gct cca gaa ggt ttt agc caa	48
Met Val His Ser Val Tyr Asn Ser Leu Ala Pro Glu Gly Phe Ser Gln	
1 5 10 15	

gtc tct att caa ccc agt cag att cca acc agc aaa aaa gta atg att	96
Val Ser Ile Gln Pro Ser Gln Ile Pro Thr Ser Lys Lys Val Met Ile	
20 25 30	

gcg ata atg act ctt ttt gca ctc aca gcc att gca gca ata gtc ctt	144
Ala Ile Met Thr Leu Phe Ala Leu Thr Ala Ile Ala Ala Ile Val Leu	
35 40 45	

tcc atc gtt aca gtt tgt gga ggg ttt cct ttt ctt ctt gct gca ctt	192
Ser Ile Val Thr Val Cys Gly Gly Phe Pro Phe Leu Leu Ala Ala Leu	
50 55 60	

aac acc gta act att ggt gca tgc gta tcc ttg ccg gta ttc act tgc	240
Asn Thr Val Thr Ile Gly Ala Cys Val Ser Leu Pro Val Phe Thr Cys	
65 70 75 80	

ata gct aca acg tta tta ctt ctt tgt ctc cgt aat atc gaa ctc cta 288

Ile Ala Thr Thr Leu Leu Leu Cys Leu Arg Asn Ile Glu Leu Leu
85 90 95

```

gcc aga ccg caa gta ttt acc ctc tcc act caa ttc agc cca aca aaa 336
Ala Arg Pro Gln Val Phe Thr Leu Ser Thr Gln Phe Ser Pro Thr Lys
100          105          110

```

cct caa gaa tag
Pro Gln Glu
115

<210> 16
<211> 115
<212> PRT
<213> Chlamydia trachomatis

<400> 16
Met Val His Ser Val Tyr Asn Ser Leu Ala Pro Glu Gly Phe Ser Gln
1 5 10 15

Val Ser Ile Gln Pro Ser Gln Ile Pro Thr Ser Lys Lys Val Met Ile
20 25 30

Ala Ile Met Thr Leu Phe Ala Leu Thr Ala Ile Ala Ala Ile Val Leu
35 40 45

Ser Ile Val Thr Val Cys Gly Gly Phe Pro Phe Leu Leu Ala Ala Leu
50 55 60

Asn	Thr	Val	Thr	Ile	Gly	Ala	Cys	Val	Ser	Leu	Pro	Val	Phe	Thr	Cys
65				70						75					80

Ile Ala Thr Thr Leu Leu Leu Leu Cys Leu Arg Asn Ile Glu Leu Leu
85 90 95

Ala Arg Pro Gln Val Phe Thr Leu Ser Thr Gln Phe Ser Pro Thr Lys
100 105 110

Pro Gln Glu
115

<210> 17
<211> 537
<212> DNA
<213> Chlamydia trachomatis

<220>
<221> CDS
<222> (1)..(537)

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<400> 17
atg acg tac tct ata tcc gat ata gca cac aaa tct gat att tct aat 48
Met Thr Tyr Ser Ile Ser Asp Ile Ala His Lys Ser Asp Ile Ser Asn
           1          5          10          15

```

```

ccc acg tct ccc gct cca tca aga aaa cga gga tcc ttt ccc cca caa 96
Pro Thr Ser Pro Ala Pro Ser Arg Lys Arg Gly Ser Phe Pro Pro Gln
          20           25           30

```

tct cct tct gcc qtg ggc tct tta gag gga gct aat ttc tct aca tgg	144																																																																																																																																																				
Ser Pro Ser Ala Val Gly Ser Leu Glu Gly Ala Asn Phe Ser Thr Trp																																																																																																																																																					
35	40		45			ggg cca ggc ccc ttc act gtc cct gtt tat cca caa caa ctc gct	192	Gly Pro Gly Pro Phe Phe Thr Val Pro Val Tyr Pro Gln Gln Leu Ala		50	55		60			gca atg caa aac aac ctt ttt aca ttg caa aca gag gtt tct gct ctc	240	Ala Met Gln Asn Asn Leu Phe Thr Leu Gln Thr Glu Val Ser Ala Leu		65	70		75		80			aag aaa aaa tta gtt cag tct agt cag aca cgc gga tct tta gga ctc	288	Lys Lys Lys Leu Val Gln Ser Ser Gln Thr Arg Gly Ser Leu Gly Leu		85	90		95			ggc ccg cag ttt tta gcg gca tgc tta gtt gct gcg aca atc ctt gca	336	Gly Pro Gln Phe Leu Ala Ala Cys Leu Val Ala Ala Thr Ile Leu Ala		100	105		110			gta gct gtt atc gta ctt gct tcc tta gga ctt ggc ggt gtt ctt cct	384	Val Ala Val Ile Val Leu Ala Ser Leu Gly Leu Gly Val Leu Pro		115	120		125			ttt gtc ctt gtt tgt ctg gct ggg tca act aat gca att tgg gct att	432	Phe Val Leu Val Cys Leu Ala Gly Ser Thr Asn Ala Ile Trp Ala Ile		130	135		140			gtg agc gcc tcc atc act aca ctg att tgt tgc gtt tcc atc gct tgc	480	Val Ser Ala Ser Ile Thr Thr Leu Ile Cys Cys Val Ser Ile Ala Cys		145	150		155		160			atc ttc tta gca aaa tgt gat aag gga tct gat cct caa act tta tat	528	Ile Phe Leu Ala Lys Cys Asp Lys Gly Ser Asp Pro Gln Thr Leu Tyr		165	170		175			gta agc taa	537	Val Ser				<210> 18		<211> 178		<212> PRT		<213> Chlamydia trachomatis				<400> 18		Met Thr Tyr Ser Ile Ser Asp Ile Ala His Lys Ser Asp Ile Ser Asn		1	5		10		15			Pro Thr Ser Pro Ala Pro Ser Arg Lys Arg Gly Ser Phe Pro Pro Gln		20	25		30			Ser Pro Ser Ala Val Gly Ser Leu Glu Gly Ala Asn Phe Ser Thr Trp		35	40		45			Gly Pro Gly Pro Phe Phe Thr Val Pro Val Tyr Pro Gln Gln Leu Ala		50	55		60			Ala Met Gln Asn Asn Leu Phe Thr Leu Gln Thr Glu Val Ser Ala Leu		65	70		75		80
	45																																																																																																																																																				
ggg cca ggc ccc ttc act gtc cct gtt tat cca caa caa ctc gct	192																																																																																																																																																				
Gly Pro Gly Pro Phe Phe Thr Val Pro Val Tyr Pro Gln Gln Leu Ala																																																																																																																																																					
50	55		60			gca atg caa aac aac ctt ttt aca ttg caa aca gag gtt tct gct ctc	240	Ala Met Gln Asn Asn Leu Phe Thr Leu Gln Thr Glu Val Ser Ala Leu		65	70		75		80			aag aaa aaa tta gtt cag tct agt cag aca cgc gga tct tta gga ctc	288	Lys Lys Lys Leu Val Gln Ser Ser Gln Thr Arg Gly Ser Leu Gly Leu		85	90		95			ggc ccg cag ttt tta gcg gca tgc tta gtt gct gcg aca atc ctt gca	336	Gly Pro Gln Phe Leu Ala Ala Cys Leu Val Ala Ala Thr Ile Leu Ala		100	105		110			gta gct gtt atc gta ctt gct tcc tta gga ctt ggc ggt gtt ctt cct	384	Val Ala Val Ile Val Leu Ala Ser Leu Gly Leu Gly Val Leu Pro		115	120		125			ttt gtc ctt gtt tgt ctg gct ggg tca act aat gca att tgg gct att	432	Phe Val Leu Val Cys Leu Ala Gly Ser Thr Asn Ala Ile Trp Ala Ile		130	135		140			gtg agc gcc tcc atc act aca ctg att tgt tgc gtt tcc atc gct tgc	480	Val Ser Ala Ser Ile Thr Thr Leu Ile Cys Cys Val Ser Ile Ala Cys		145	150		155		160			atc ttc tta gca aaa tgt gat aag gga tct gat cct caa act tta tat	528	Ile Phe Leu Ala Lys Cys Asp Lys Gly Ser Asp Pro Gln Thr Leu Tyr		165	170		175			gta agc taa	537	Val Ser				<210> 18		<211> 178		<212> PRT		<213> Chlamydia trachomatis				<400> 18		Met Thr Tyr Ser Ile Ser Asp Ile Ala His Lys Ser Asp Ile Ser Asn		1	5		10		15			Pro Thr Ser Pro Ala Pro Ser Arg Lys Arg Gly Ser Phe Pro Pro Gln		20	25		30			Ser Pro Ser Ala Val Gly Ser Leu Glu Gly Ala Asn Phe Ser Thr Trp		35	40		45			Gly Pro Gly Pro Phe Phe Thr Val Pro Val Tyr Pro Gln Gln Leu Ala		50	55		60			Ala Met Gln Asn Asn Leu Phe Thr Leu Gln Thr Glu Val Ser Ala Leu		65	70		75		80										
	60																																																																																																																																																				
gca atg caa aac aac ctt ttt aca ttg caa aca gag gtt tct gct ctc	240																																																																																																																																																				
Ala Met Gln Asn Asn Leu Phe Thr Leu Gln Thr Glu Val Ser Ala Leu																																																																																																																																																					
65	70		75		80			aag aaa aaa tta gtt cag tct agt cag aca cgc gga tct tta gga ctc	288	Lys Lys Lys Leu Val Gln Ser Ser Gln Thr Arg Gly Ser Leu Gly Leu		85	90		95			ggc ccg cag ttt tta gcg gca tgc tta gtt gct gcg aca atc ctt gca	336	Gly Pro Gln Phe Leu Ala Ala Cys Leu Val Ala Ala Thr Ile Leu Ala		100	105		110			gta gct gtt atc gta ctt gct tcc tta gga ctt ggc ggt gtt ctt cct	384	Val Ala Val Ile Val Leu Ala Ser Leu Gly Leu Gly Val Leu Pro		115	120		125			ttt gtc ctt gtt tgt ctg gct ggg tca act aat gca att tgg gct att	432	Phe Val Leu Val Cys Leu Ala Gly Ser Thr Asn Ala Ile Trp Ala Ile		130	135		140			gtg agc gcc tcc atc act aca ctg att tgt tgc gtt tcc atc gct tgc	480	Val Ser Ala Ser Ile Thr Thr Leu Ile Cys Cys Val Ser Ile Ala Cys		145	150		155		160			atc ttc tta gca aaa tgt gat aag gga tct gat cct caa act tta tat	528	Ile Phe Leu Ala Lys Cys Asp Lys Gly Ser Asp Pro Gln Thr Leu Tyr		165	170		175			gta agc taa	537	Val Ser				<210> 18		<211> 178		<212> PRT		<213> Chlamydia trachomatis				<400> 18		Met Thr Tyr Ser Ile Ser Asp Ile Ala His Lys Ser Asp Ile Ser Asn		1	5		10		15			Pro Thr Ser Pro Ala Pro Ser Arg Lys Arg Gly Ser Phe Pro Pro Gln		20	25		30			Ser Pro Ser Ala Val Gly Ser Leu Glu Gly Ala Asn Phe Ser Thr Trp		35	40		45			Gly Pro Gly Pro Phe Phe Thr Val Pro Val Tyr Pro Gln Gln Leu Ala		50	55		60			Ala Met Gln Asn Asn Leu Phe Thr Leu Gln Thr Glu Val Ser Ala Leu		65	70		75		80																				
	75		80			aag aaa aaa tta gtt cag tct agt cag aca cgc gga tct tta gga ctc	288	Lys Lys Lys Leu Val Gln Ser Ser Gln Thr Arg Gly Ser Leu Gly Leu		85	90		95			ggc ccg cag ttt tta gcg gca tgc tta gtt gct gcg aca atc ctt gca	336	Gly Pro Gln Phe Leu Ala Ala Cys Leu Val Ala Ala Thr Ile Leu Ala		100	105		110			gta gct gtt atc gta ctt gct tcc tta gga ctt ggc ggt gtt ctt cct	384	Val Ala Val Ile Val Leu Ala Ser Leu Gly Leu Gly Val Leu Pro		115	120		125			ttt gtc ctt gtt tgt ctg gct ggg tca act aat gca att tgg gct att	432	Phe Val Leu Val Cys Leu Ala Gly Ser Thr Asn Ala Ile Trp Ala Ile		130	135		140			gtg agc gcc tcc atc act aca ctg att tgt tgc gtt tcc atc gct tgc	480	Val Ser Ala Ser Ile Thr Thr Leu Ile Cys Cys Val Ser Ile Ala Cys		145	150		155		160			atc ttc tta gca aaa tgt gat aag gga tct gat cct caa act tta tat	528	Ile Phe Leu Ala Lys Cys Asp Lys Gly Ser Asp Pro Gln Thr Leu Tyr		165	170		175			gta agc taa	537	Val Ser				<210> 18		<211> 178		<212> PRT		<213> Chlamydia trachomatis				<400> 18		Met Thr Tyr Ser Ile Ser Asp Ile Ala His Lys Ser Asp Ile Ser Asn		1	5		10		15			Pro Thr Ser Pro Ala Pro Ser Arg Lys Arg Gly Ser Phe Pro Pro Gln		20	25		30			Ser Pro Ser Ala Val Gly Ser Leu Glu Gly Ala Asn Phe Ser Thr Trp		35	40		45			Gly Pro Gly Pro Phe Phe Thr Val Pro Val Tyr Pro Gln Gln Leu Ala		50	55		60			Ala Met Gln Asn Asn Leu Phe Thr Leu Gln Thr Glu Val Ser Ala Leu		65	70		75		80																						
	80																																																																																																																																																				
aag aaa aaa tta gtt cag tct agt cag aca cgc gga tct tta gga ctc	288																																																																																																																																																				
Lys Lys Lys Leu Val Gln Ser Ser Gln Thr Arg Gly Ser Leu Gly Leu																																																																																																																																																					
85	90		95			ggc ccg cag ttt tta gcg gca tgc tta gtt gct gcg aca atc ctt gca	336	Gly Pro Gln Phe Leu Ala Ala Cys Leu Val Ala Ala Thr Ile Leu Ala		100	105		110			gta gct gtt atc gta ctt gct tcc tta gga ctt ggc ggt gtt ctt cct	384	Val Ala Val Ile Val Leu Ala Ser Leu Gly Leu Gly Val Leu Pro		115	120		125			ttt gtc ctt gtt tgt ctg gct ggg tca act aat gca att tgg gct att	432	Phe Val Leu Val Cys Leu Ala Gly Ser Thr Asn Ala Ile Trp Ala Ile		130	135		140			gtg agc gcc tcc atc act aca ctg att tgt tgc gtt tcc atc gct tgc	480	Val Ser Ala Ser Ile Thr Thr Leu Ile Cys Cys Val Ser Ile Ala Cys		145	150		155		160			atc ttc tta gca aaa tgt gat aag gga tct gat cct caa act tta tat	528	Ile Phe Leu Ala Lys Cys Asp Lys Gly Ser Asp Pro Gln Thr Leu Tyr		165	170		175			gta agc taa	537	Val Ser				<210> 18		<211> 178		<212> PRT		<213> Chlamydia trachomatis				<400> 18		Met Thr Tyr Ser Ile Ser Asp Ile Ala His Lys Ser Asp Ile Ser Asn		1	5		10		15			Pro Thr Ser Pro Ala Pro Ser Arg Lys Arg Gly Ser Phe Pro Pro Gln		20	25		30			Ser Pro Ser Ala Val Gly Ser Leu Glu Gly Ala Asn Phe Ser Thr Trp		35	40		45			Gly Pro Gly Pro Phe Phe Thr Val Pro Val Tyr Pro Gln Gln Leu Ala		50	55		60			Ala Met Gln Asn Asn Leu Phe Thr Leu Gln Thr Glu Val Ser Ala Leu		65	70		75		80																																
	95																																																																																																																																																				
ggc ccg cag ttt tta gcg gca tgc tta gtt gct gcg aca atc ctt gca	336																																																																																																																																																				
Gly Pro Gln Phe Leu Ala Ala Cys Leu Val Ala Ala Thr Ile Leu Ala																																																																																																																																																					
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gta gct gtt atc gta ctt gct tcc tta gga ctt ggc ggt gtt ctt cct	384																																																																																																																																																				
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Ser Pro Ser Ala Val Gly Ser Leu Glu Gly Ala Asn Phe Ser Thr Trp																																																																																																																																																					
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Gly Pro Gly Pro Phe Phe Thr Val Pro Val Tyr Pro Gln Gln Leu Ala																																																																																																																																																					
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Ala Met Gln Asn Asn Leu Phe Thr Leu Gln Thr Glu Val Ser Ala Leu																																																																																																																																																					
65	70		75		80																																																																																																																																																
	75		80																																																																																																																																																		
	80																																																																																																																																																				

Lys Lys Lys Leu Val Gln Ser Ser Gln Thr Arg Gly Ser Leu Gly Leu
85 90 95

Gly Pro Gln Phe Leu Ala Ala Cys Leu Val Ala Ala Thr Ile Leu Ala
100 105 110

Val Ala Val Ile Val Leu Ala Ser Leu Gly Leu Gly Gly Val Leu Pro
115 120 125

Phe Val Leu Val Cys Leu Ala Gly Ser Thr Asn Ala Ile Trp Ala Ile
130 135 140

Val Ser Ala Ser Ile Thr Thr Leu Ile Cys Cys Val Ser Ile Ala Cys
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Ile Phe Leu Ala Lys Cys Asp Lys Gly Ser Asp Pro Gln Thr Leu Tyr
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Val Ser

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26

09/673763

532 Rec'd PCT/PTC 16 OCT 2000

WO 99/53948

PCT/US99/08744

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INCC proteins of Chlamydia

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<151> 1998-04-21

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1				5					10							15	

aca	ttt	gca	gct	aat	tct	aca	ggc	aca	att	gga	atc	gtt	aat	tta	cgt		96
Thr	Phe	Ala	Ala	Asn	Ser	Thr	Gly	Thr	Ile	Gly	Ile	Val	Asn	Leu	Arg		
20						25									30		

cgc	tgc	cta	gaa	gag	tct	gct	ctt	ggg	aaa	aaa	gaa	tct	gct	gaa	ttc		144
Arg	Cys	Leu	Glu	Glu	Ser	Ala	Leu	Gly	Lys	Lys	Glu	Ser	Ala	Glu	Phe		
35						40									45		

gaa	aag	atg	aaa	aac	caa	ttc	tct	aac	agc	atg	ggg	aag	atg	gag	gaa		192
Glu	Lys	Met	Lys	Asn	Gln	Phe	Ser	Asn	Ser	Met	Gly	Lys	Met	Glu	Glu		
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gaa	ctg	tct	tct	tat	tcc	aag	ctc	caa	gac	gac	gat	tac	atg	gaa		240	
Glu	Leu	Ser	Ser	Ile	Tyr	Ser	Lys	Leu	Gln	Asp	Asp	Asp	Tyr	Met	Glu		
65				70					75				80		80		

ggt	cta	tcc	gag	acc	gca	gct	gcc	gaa	tta	aga	aaa	aaa	tcc	gaa	gat		288
Gly	Leu	Ser	Glu	Thr	Ala	Ala	Glu	Leu	Arg	Lys	Lys	Phe	Glu	Asp			
85							90							95			

cta	tct	gca	gaa	tac	aac	aca	gct	caa	ggg	cag	tat	tac	caa	ata	tta		336
Leu	Ser	Ala	Glu	Tyr	Asn	Thr	Ala	Ala	Glu	Leu	Arg	Lys	Phe	Glu	Asp		

100

105

110

aac caa agt aat ttc aag cgc atg caa aag att atg gaa gaa gtg aaa	384		
Asn Gln Ser Asn Phe Lys Arg Met Gln Lys Ile Met Glu Glu Val Lys			
115	120		125
	125		

aaa gct tct gaa act gtg cgt att caa gaa ggc ttg tca gtc ctt ctt	432		
Lys Ala Ser Glu Thr Val Arg Ile Gln Glu Gly Leu Ser Val Leu Leu			
130	135		140
	140		

aac gaa gat att gtc tta tct atc gat agt tcg gca gat aaa acc gat	480				
Asn Glu Asp Ile Val Leu Ser Ile Asp Ser Ser Ala Asp Lys Thr Asp					
145	150		155		160
	155		160		
	160				

gct gtt att aaa gtt ctt gat gtt ctt ttc aaa ata att aac atg cga	528		
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165	170		175
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agc tag	534
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	30		

Arg Cys Leu Glu Glu Ser Ala Leu Gly Lys Lys Glu Ser Ala Glu Phe			
35	40		45
	45		

Glu Lys Met Lys Asn Gln Phe Ser Asn Ser Met Gly Lys Met Glu Glu			
50	55		60
	60		

Glu Leu Ser Ser Ile Tyr Ser Lys Leu Gln Asp Asp Asp Tyr Met Glu					
65	70		75		80
	75		80		
	80				

Gly Leu Ser Glu Thr Ala Ala Ala Glu Leu Arg Lys Lys Phe Glu Asp			
85	90		95
	95		

Leu Ser Ala Glu Tyr Asn Thr Ala Gln Gly Gln Tyr Tyr Gln Ile Leu			
100	105		110
	110		

Asn Gln Ser Asn Phe Lys Arg Met Gln Lys Ile Met Glu Glu Val Lys			
115	120		125
	125		

Lys Ala Ser Glu Thr Val Arg Ile Gln Glu Gly Leu Ser Val Leu Leu			
130	135		140
	140		

Asn Glu Asp Ile Val Leu Ser Ile Asp Ser Ser Ala Asp Lys Thr Asp					
145	150		155		160
	155		160		
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Ala Val Ile Lys Val Leu Asp Val Leu Phe Lys Ile Ile Asn Met Arg			
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	175		

Ser

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gtc aag aat att gtt ctg att gat gga gcg att gat cct cat tca tat 96
Val Lys Asn Ile Val Leu Ile Asp Gly Ala Ile Asp Pro His Ser Tyr
20 25 30

gag atg gtg aag ggg gat gaa gac cga atg gct atg agc cag ctg att 144
Glu Met Val Lys Gly Asp Glu Asp Arg Met Ala Met Ser Gln Leu Ile
35 40 45

ttt tgc aat ggt tta ggt tta gag cat tca gct agt tta cgt aaa cat 192
Phe Cys Asn Gly Leu Gly Leu Glu His Ser Ala Ser Leu Arg Lys His
50 55 60

cta gag ggt aac cca aaa gtc gtt gat tta ggt caa cgt ttg ctt aac 240
Leu Glu Gly Asn Pro Lys Val Val Asp Leu Gly Gln Arg Leu Leu Asn
65 70 75 80

aaa aac tgt ttt gat ctt ctg agt gaa gaa gga ttc cct gac cca cat 288
Lys Asn Cys Phe Asp Leu Leu Ser Glu Glu Gly Phe Pro Asp Pro His
85 90 95

att tgg acg gat atg aga gta tgg ggt gct gct gta aaa gag atg gct 336
Ile Trp Thr Asp Met Arg Val Trp Gly Ala Ala Val Lys Glu Met Ala
100 105 110

gcg gca tta att caa caa ttt cct caa tat gaa gaa gat ttt caa aag 384
Ala Ala Leu Ile Gln Gln Phe Pro Gln Tyr Glu Glu Asp Phe Gln Lys
115 120 125

aat gcg gat cag atc tta tca gag atg gag gaa ctt gat cgt tgg gca 432
Asn Ala Asp Gln Ile Leu Ser Glu Met Glu Glu Leu Asp Arg Trp Ala
130 135 140

gtc cgt tct ctc tct acg att cct gaa aaa aat cgc tat tta gtc aca 480
Val Arg Ser Leu Ser Thr Ile Pro Glu Lys Asn Arg Tyr Leu Val Thr
145 150 155 160

ggc cac aat gcg ttc agt tac ttt act cgt cgg tat cta tcc tct gat 528
Gly His Asn Ala Phe Ser Tyr Phe Thr Arg Arg Tyr Leu Ser Ser Asp
165 170 175

gcg gag aga gtg tct ggg gaa tgg aga tcg cgt tgc att tct cca gaa 576
Ala Glu Arg Val Ser Gly Glu Trp Arg Ser Arg Cys Ile Ser Pro Glu
180 185 190

ggg ttg tct cct gag gct cag att agt atc cga gat att atg cgt gta 624
 Gly Leu Ser Pro Glu Ala Gln Ile Ser Ile Arg Asp Ile Met Arg Val
 195 200 205

gtg gag tat atc tct gca aac gat gta gaa gtt gtc ttt tta gag gat 672
 Val Glu Tyr Ile Ser Ala Asn Asp Val Glu Val Val Phe Leu Glu Asp
 210 215 220

acg tta aat caa gat gct ttg aga aag att gtt tct tgc tct aag agc 720
 Thr Leu Asn Gln Asp Ala Leu Arg Lys Ile Val Ser Cys Ser Lys Ser
 225 230 235 240

gga caa aag att cgt ctc gct aag tct cct tta tat agc gat aat gtc 768
 Gly Gln Lys Ile Arg Leu Ala Lys Ser Pro Leu Tyr Ser Asp Asn Val
 245 250 255

tgt gat aac tat ttt agc acg ttc cag cac aat gtt cgc aca att aca 816
 Cys Asp Asn Tyr Phe Ser Thr Phe Gln His Asn Val Arg Thr Ile Thr
 260 265 270

gaa gaa ttg gga ggg act gtt ctt gaa tag 846
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Glu Met Val Lys Gly Asp Glu Asp Arg Met Ala Met Ser Gln Leu Ile
 35 40 45

Phe Cys Asn Gly Leu Gly Leu Glu His Ser Ala Ser Leu Arg Lys His
 50 55 60

Leu Glu Gly Asn Pro Lys Val Val Asp Leu Gly Gln Arg Leu Leu Asn
 65 70 75 80

Lys Asn Cys Phe Asp Leu Leu Ser Glu Glu Gly Phe Pro Asp Pro His
 85 90 95

Ile Trp Thr Asp Met Arg Val Trp Gly Ala Ala Val Lys Glu Met Ala
 100 105 110

Ala Ala Leu Ile Gln Gln Phe Pro Gln Tyr Glu Glu Asp Phe Gln Lys
 115 120 125

Asn Ala Asp Gln Ile Leu Ser Glu Met Glu Glu Leu Asp Arg Trp Ala
 130 135 140

Val Arg Ser Leu Ser Thr Ile Pro Glu Lys Asn Arg Tyr Leu Val Thr
 145 150 155 160

WO 99/53948

PCT/US99/08744

Gly His Asn Ala Phe Ser Tyr Phe Thr Arg Arg Tyr Leu Ser Ser Asp
165 170

Ala Glu Arg Val Ser Gly Glu Trp Arg Ser Arg Cys Ile Ser Pro Glu
180 185 190

Gly Leu Ser Pro Glu Ala Gln Ile Ser Ile Arg Asp Ile Met Arg Val
195 200 205

Val Glu Tyr Ile Ser Ala Asn Asp Val Glu Val Val Phe Leu Glu Asp
210 215 220

Thr Leu Asn Gln Asp Ala Leu Arg Lys Ile Val Ser Cys Ser Lys Ser
225 230 235 240

Gly Gln Lys Ile Arg Leu Ala Lys Ser Pro Leu Tyr Ser Asp Asn Val
245 250 255

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260 265 270

Glu Glu Leu Gly Gly Thr Val Leu Glu
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tta cag aat tgg gag gga ctg ttc ttg aat aga gat aat gca att 96
Leu Gln Lys Asn Trp Glu Gly Leu Phe Leu Asn Arg Asp Asn Ala Ile
20 25 30

gct tgg tcc gta gag gat ctt tgt gtt aat tat gat cac tca gac gtc 144
Ala Trp Ser Val Glu Asp Leu Cys Val Asn Tyr Asp His Ser Asp Val
35 40 45

tta tgt cac att act ttt tct ctg cct gca ggg gca atg gct gct att 192
Leu Cys His Ile Thr Phe Ser Leu Pro Ala Gly Ala Met Ala Ala Ile
50 55 60

att ggg ccg aat gga gct ggt aaa agt act ttg ctt aag gct tct tta 240
Ile Gly Pro Asn Gly Ala Gly Lys Ser Thr Leu Leu Lys Ala Ser Leu
65 70 75 80

gga ctg att cgt gct tct tct ggc caa agc ttg ttc ttt ggt cag aga 288
Gly Leu Ile Arg Ala Ser Ser Gly Gln Ser Leu Phe Phe Gly Gln Arg
85 90 95

ttt tcc aag gca cat cat aga ata gcc tat atg cct caa aga gcg agt 336
Phe Ser Lys Ala His His Arg Ile Ala Tyr Met Pro Gln Arg Ala Ser

100	105	110	
gtg gat tgg gat ttc cca atg act gtt ctt gat ctc gtg ttg atg ggg Val Asp Trp Asp Phe Pro Met Thr Val Leu Asp Leu Val Leu Met Gly	115	120	384
		125	
tgt tac ggc tat aaa gga ata tgg aat cgt att tcc act gat gat cgt Cys Tyr Gly Tyr Lys Gly Ile Trp Asn Arg Ile Ser Thr Asp Asp Arg	130	135	432
		140	
cag gag gct atg cgt att tta gag cgg gtt ggt gaa gct ttt gca Gln Ala Glu Ala Met Arg Ile Leu Glu Arg Val Gly Leu Glu Ala Phe Ala	145	150	480
		155	
aat cgt caa ata ggt aag ctc tct gga gga caa caa cag aga gct ttt Asn Arg Gln Ile Gly Lys Leu Ser Gly Gly Gln Gln Gln Arg Ala Phe	165	170	528
		175	
tta gcg cgg tca tta atg caa aaa gca gat ttg tat ctc atg gat gag Leu Ala Arg Ser Leu Met Gln Lys Ala Asp Leu Tyr Leu Met Asp Glu	180	185	576
		190	
ctg ttc tct gcg atc gat atg gcc tct tat cag atg gtt gta gat gtt Leu Phe Ser Ala Ile Asp Met Ala Ser Tyr Gln Met Val Val Asp Val	195	200	624
		205	
ttg caa gag ctt aaa aag gaa ggg aag act att gtg gtc att cat cat Leu Gln Glu Leu Lys Ser Glu Gly Lys Thr Ile Val Val Ile His His	210	215	672
		220	
gat ttg aat gtc cgg aag ctt ttt gat cat gtg att tta tta aat Asp Leu Ser Asn Val Arg Lys Leu Phe Asp His Val Ile Leu Asn	225	230	720
		235	
aag cat ctt gtg tgc tct gga agc gta gaa gaa tgc ttg act aaa gaa Lys His Leu Val Cys Ser Gly Ser Val Glu Glu Cys Leu Thr Lys Glu	245	250	768
		255	
gcc att ttt cag gct tat ggg tgt gac ttg agc ttt ttg att aca cac Ala Ile Phe Gln Ala Tyr Gly Cys Asp Leu Ser Phe Trp Ile Thr His	260	265	816
		270	
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		285	
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Ala Trp Ser Val Glu Asp Leu Cys Val Asn Tyr Asp His Ser Asp Val 35 40 45			

Leu Cys His Ile Thr Phe Ser Leu Pro Ala Gly Ala Met Ala Ala Ile
 50 55 60
 Ile Gly Pro Asn Gly Ala Gly Lys Ser Thr Leu Leu Lys Ala Ser Leu
 65 70 75 80
 Gly Leu Ile Arg Ala Ser Ser Gly Gln Ser Leu Phe Phe Gly Gln Arg
 85 90 95
 Phe Ser Lys Ala His His Arg Ile Ala Tyr Met Pro Gln Arg Ala Ser
 100 105 110
 Val Asp Trp Asp Phe Pro Met Thr Val Leu Asp Leu Val Leu Met Gly
 115 120 125
 Cys Tyr Gly Tyr Lys Gly Ile Trp Asn Arg Ile Ser Thr Asp Asp Arg
 130 135 140
 Gln Glu Ala Met Arg Ile Leu Glu Arg Val Gly Leu Glu Ala Phe Ala
 145 150 155 160
 Asn Arg Gln Ile Gly Lys Leu Ser Gly Gly Gln Gln Arg Ala Phe
 165 170 175
 Leu Ala Arg Ser Leu Met Gln Lys Ala Asp Leu Tyr Leu Met Asp Glu
 180 185 190
 Leu Phe Ser Ala Ile Asp Met Ala Ser Tyr Gln Met Val Val Asp Val
 195 200 205
 Leu Gln Glu Leu Lys Ser Glu Gly Lys Thr Ile Val Val Ile His His
 210 215 220
 Asp Leu Ser Asn Val Arg Lys Leu Phe Asp His Val Ile Leu Leu Asn
 225 230 235 240
 Lys His Leu Val Cys Ser Gly Ser Val Glu Glu Cys Leu Thr Lys Glu
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 Met Thr Val Ser Thr Asp Asn Thr Ser Pro Val Ile Ser Arg Ala Ser
 1 5 10 15

tca cct act ttt gga gat cat ggt aag gat ttc gac aac aat aaa att	96																																																																																																																										
Ser Pro Thr Phe Gly Asp His Gly Lys Asp Phe Asp Asn Asn Lys Ile																																																																																																																											
20	25		30	ata ccc att tca ata gaa gct cca act tct tca gct gct gct gta ggg	144	Ile Pro Ile Ser Ile Glu Ala Pro Thr Ser Ser Ala Ala Ala Val Gly		35	40		45	gct aaa acg gct atc gag cct gaa gga aga agc cca cta ctt caa agg	192	Ala Lys Thr Ala Ile Glu Pro Glu Gly Arg Ser Pro Leu Leu Gln Arg		50	55		60	att tgc tat ctt gtt aaa att atc gct gcc atc gcc ctc ttt gtt gtt	240	Ile Cys Tyr Leu Val Lys Ile Ile Ala Ala Leu Phe Val Val		65	70		75		80	ggt atc gca gcc tta gtt tgc tta tat ctc ggt agc gtt atc tca acg	288	Gly Ile Ala Ala Leu Val Cys Leu Tyr Leu Gly Ser Val Ile Ser Thr		85	90		95	cct tct ctt att ctt atg ctt gcg atc atg ctt gta tcc ttt gtg atc	336	Pro Ser Leu Ile Leu Met Leu Ala Ile Met Leu Val Ser Phe Val Ile		100	105		110	gtt att acg gca att cga gat ggc aca ccg tct caa gtg gtc cgt cac	384	Val Ile Thr Ala Ile Arg Asp Gly Thr Pro Ser Gln Val Val Arg His		115	120		125	atg aaa cag caa att cag caa ttt ggc gaa gaa aac acg cgt tta cat	432	Met Lys Gln Ile Gln Gln Phe Gly Glu Glu Asn Thr Arg Leu His		130	135		140	acc gca gta gaa aat cta aaa gct gtt aac gtt gag ctc tca gag caa	480	Thr Ala Val Glu Asn Leu Lys Ala Val Asn Val Glu Leu Ser Glu Gln		145	150		155		160	att aac caa ctt aaa caa cta cat act aga tta tcg gat ttt ggt gat	528	Ile Asn Gln Leu Gln Leu His Thr Arg Leu Ser Asp Phe Gly Asp		165	170		175	agg ctt gaa gcg aat acc ggt gat ttt act gca ctt att gcg gat ttc	576	Arg Leu Glu Ala Asn Thr Gly Asp Phe Thr Ala leu Ile Ala Asp Phe		180	185		190	caa ctc agt ctg gaa gag ttt aag tct gtt ggt act aaa gtt gaa acc	624	Gln Leu Ser Leu Glu Glu Phe Lys Ser Val Gly Thr Lys Val Glu Thr		195	200		205	atg ctc tct cca ttt gag aaa tta gct cag tct ttg aaa gag acc ttt	672	Met Leu Ser Pro Phe Glu Lys Leu Ala Gln Ser Leu Lys Glu Thr Phe		210	215		220	tct caa gaa gct gtt cag gca atg atg tcc tct gta act gag tta aga	720	Ser Gln Glu Ala Val Gln Ala Met Met Ser Ser Val Thr Glu Leu Arg		225	230		235		240	acc aat ttg aat gca ttg aaa gag ctt ata aca gag aat aaa acc gta	768	Thr Asn Leu Asn Ala leu Lys Glu Leu Ile Thr Glu Asn Lys Thr Val		245	250		255	ata gag caa cta aaa gct gat gct caa ctt aga gaa gag caa gtg cgg	816
	30																																																																																																																										
ata ccc att tca ata gaa gct cca act tct tca gct gct gct gta ggg	144																																																																																																																										
Ile Pro Ile Ser Ile Glu Ala Pro Thr Ser Ser Ala Ala Ala Val Gly																																																																																																																											
35	40		45	gct aaa acg gct atc gag cct gaa gga aga agc cca cta ctt caa agg	192	Ala Lys Thr Ala Ile Glu Pro Glu Gly Arg Ser Pro Leu Leu Gln Arg		50	55		60	att tgc tat ctt gtt aaa att atc gct gcc atc gcc ctc ttt gtt gtt	240	Ile Cys Tyr Leu Val Lys Ile Ile Ala Ala Leu Phe Val Val		65	70		75		80	ggt atc gca gcc tta gtt tgc tta tat ctc ggt agc gtt atc tca acg	288	Gly Ile Ala Ala Leu Val Cys Leu Tyr Leu Gly Ser Val Ile Ser Thr		85	90		95	cct tct ctt att ctt atg ctt gcg atc atg ctt gta tcc ttt gtg atc	336	Pro Ser Leu Ile Leu Met Leu Ala Ile Met Leu Val Ser Phe Val Ile		100	105		110	gtt att acg gca att cga gat ggc aca ccg tct caa gtg gtc cgt cac	384	Val Ile Thr Ala Ile Arg Asp Gly Thr Pro Ser Gln Val Val Arg His		115	120		125	atg aaa cag caa att cag caa ttt ggc gaa gaa aac acg cgt tta cat	432	Met Lys Gln Ile Gln Gln Phe Gly Glu Glu Asn Thr Arg Leu His		130	135		140	acc gca gta gaa aat cta aaa gct gtt aac gtt gag ctc tca gag caa	480	Thr Ala Val Glu Asn Leu Lys Ala Val Asn Val Glu Leu Ser Glu Gln		145	150		155		160	att aac caa ctt aaa caa cta cat act aga tta tcg gat ttt ggt gat	528	Ile Asn Gln Leu Gln Leu His Thr Arg Leu Ser Asp Phe Gly Asp		165	170		175	agg ctt gaa gcg aat acc ggt gat ttt act gca ctt att gcg gat ttc	576	Arg Leu Glu Ala Asn Thr Gly Asp Phe Thr Ala leu Ile Ala Asp Phe		180	185		190	caa ctc agt ctg gaa gag ttt aag tct gtt ggt act aaa gtt gaa acc	624	Gln Leu Ser Leu Glu Glu Phe Lys Ser Val Gly Thr Lys Val Glu Thr		195	200		205	atg ctc tct cca ttt gag aaa tta gct cag tct ttg aaa gag acc ttt	672	Met Leu Ser Pro Phe Glu Lys Leu Ala Gln Ser Leu Lys Glu Thr Phe		210	215		220	tct caa gaa gct gtt cag gca atg atg tcc tct gta act gag tta aga	720	Ser Gln Glu Ala Val Gln Ala Met Met Ser Ser Val Thr Glu Leu Arg		225	230		235		240	acc aat ttg aat gca ttg aaa gag ctt ata aca gag aat aaa acc gta	768	Thr Asn Leu Asn Ala leu Lys Glu Leu Ile Thr Glu Asn Lys Thr Val		245	250		255	ata gag caa cta aaa gct gat gct caa ctt aga gaa gag caa gtg cgg	816								
	45																																																																																																																										
gct aaa acg gct atc gag cct gaa gga aga agc cca cta ctt caa agg	192																																																																																																																										
Ala Lys Thr Ala Ile Glu Pro Glu Gly Arg Ser Pro Leu Leu Gln Arg																																																																																																																											
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	60																																																																																																																										
att tgc tat ctt gtt aaa att atc gct gcc atc gcc ctc ttt gtt gtt	240																																																																																																																										
Ile Cys Tyr Leu Val Lys Ile Ile Ala Ala Leu Phe Val Val																																																																																																																											
65	70		75		80	ggt atc gca gcc tta gtt tgc tta tat ctc ggt agc gtt atc tca acg	288	Gly Ile Ala Ala Leu Val Cys Leu Tyr Leu Gly Ser Val Ile Ser Thr		85	90		95	cct tct ctt att ctt atg ctt gcg atc atg ctt gta tcc ttt gtg atc	336	Pro Ser Leu Ile Leu Met Leu Ala Ile Met Leu Val Ser Phe Val Ile		100	105		110	gtt att acg gca att cga gat ggc aca ccg tct caa gtg gtc cgt cac	384	Val Ile Thr Ala Ile Arg Asp Gly Thr Pro Ser Gln Val Val Arg His		115	120		125	atg aaa cag caa att cag caa ttt ggc gaa gaa aac acg cgt tta cat	432	Met Lys Gln Ile Gln Gln Phe Gly Glu Glu Asn Thr Arg Leu His		130	135		140	acc gca gta gaa aat cta aaa gct gtt aac gtt gag ctc tca gag caa	480	Thr Ala Val Glu Asn Leu Lys Ala Val Asn Val Glu Leu Ser Glu Gln		145	150		155		160	att aac caa ctt aaa caa cta cat act aga tta tcg gat ttt ggt gat	528	Ile Asn Gln Leu Gln Leu His Thr Arg Leu Ser Asp Phe Gly Asp		165	170		175	agg ctt gaa gcg aat acc ggt gat ttt act gca ctt att gcg gat ttc	576	Arg Leu Glu Ala Asn Thr Gly Asp Phe Thr Ala leu Ile Ala Asp Phe		180	185		190	caa ctc agt ctg gaa gag ttt aag tct gtt ggt act aaa gtt gaa acc	624	Gln Leu Ser Leu Glu Glu Phe Lys Ser Val Gly Thr Lys Val Glu Thr		195	200		205	atg ctc tct cca ttt gag aaa tta gct cag tct ttg aaa gag acc ttt	672	Met Leu Ser Pro Phe Glu Lys Leu Ala Gln Ser Leu Lys Glu Thr Phe		210	215		220	tct caa gaa gct gtt cag gca atg atg tcc tct gta act gag tta aga	720	Ser Gln Glu Ala Val Gln Ala Met Met Ser Ser Val Thr Glu Leu Arg		225	230		235		240	acc aat ttg aat gca ttg aaa gag ctt ata aca gag aat aaa acc gta	768	Thr Asn Leu Asn Ala leu Lys Glu Leu Ile Thr Glu Asn Lys Thr Val		245	250		255	ata gag caa cta aaa gct gat gct caa ctt aga gaa gag caa gtg cgg	816																								
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cct tct ctt att ctt atg ctt gcg atc atg ctt gta tcc ttt gtg atc	336																																																																																																																										
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Val Ile Thr Ala Ile Arg Asp Gly Thr Pro Ser Gln Val Val Arg His																																																																																																																											
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	125																																																																																																																										
atg aaa cag caa att cag caa ttt ggc gaa gaa aac acg cgt tta cat	432																																																																																																																										
Met Lys Gln Ile Gln Gln Phe Gly Glu Glu Asn Thr Arg Leu His																																																																																																																											
130	135		140	acc gca gta gaa aat cta aaa gct gtt aac gtt gag ctc tca gag caa	480	Thr Ala Val Glu Asn Leu Lys Ala Val Asn Val Glu Leu Ser Glu Gln		145	150		155		160	att aac caa ctt aaa caa cta cat act aga tta tcg gat ttt ggt gat	528	Ile Asn Gln Leu Gln Leu His Thr Arg Leu Ser Asp Phe Gly Asp		165	170		175	agg ctt gaa gcg aat acc ggt gat ttt act gca ctt att gcg gat ttc	576	Arg Leu Glu Ala Asn Thr Gly Asp Phe Thr Ala leu Ile Ala Asp Phe		180	185		190	caa ctc agt ctg gaa gag ttt aag tct gtt ggt act aaa gtt gaa acc	624	Gln Leu Ser Leu Glu Glu Phe Lys Ser Val Gly Thr Lys Val Glu Thr		195	200		205	atg ctc tct cca ttt gag aaa tta gct cag tct ttg aaa gag acc ttt	672	Met Leu Ser Pro Phe Glu Lys Leu Ala Gln Ser Leu Lys Glu Thr Phe		210	215		220	tct caa gaa gct gtt cag gca atg atg tcc tct gta act gag tta aga	720	Ser Gln Glu Ala Val Gln Ala Met Met Ser Ser Val Thr Glu Leu Arg		225	230		235		240	acc aat ttg aat gca ttg aaa gag ctt ata aca gag aat aaa acc gta	768	Thr Asn Leu Asn Ala leu Lys Glu Leu Ile Thr Glu Asn Lys Thr Val		245	250		255	ata gag caa cta aaa gct gat gct caa ctt aga gaa gag caa gtg cgg	816																																																										
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acc gca gta gaa aat cta aaa gct gtt aac gtt gag ctc tca gag caa	480																																																																																																																										
Thr Ala Val Glu Asn Leu Lys Ala Val Asn Val Glu Leu Ser Glu Gln																																																																																																																											
145	150		155		160	att aac caa ctt aaa caa cta cat act aga tta tcg gat ttt ggt gat	528	Ile Asn Gln Leu Gln Leu His Thr Arg Leu Ser Asp Phe Gly Asp		165	170		175	agg ctt gaa gcg aat acc ggt gat ttt act gca ctt att gcg gat ttc	576	Arg Leu Glu Ala Asn Thr Gly Asp Phe Thr Ala leu Ile Ala Asp Phe		180	185		190	caa ctc agt ctg gaa gag ttt aag tct gtt ggt act aaa gtt gaa acc	624	Gln Leu Ser Leu Glu Glu Phe Lys Ser Val Gly Thr Lys Val Glu Thr		195	200		205	atg ctc tct cca ttt gag aaa tta gct cag tct ttg aaa gag acc ttt	672	Met Leu Ser Pro Phe Glu Lys Leu Ala Gln Ser Leu Lys Glu Thr Phe		210	215		220	tct caa gaa gct gtt cag gca atg atg tcc tct gta act gag tta aga	720	Ser Gln Glu Ala Val Gln Ala Met Met Ser Ser Val Thr Glu Leu Arg		225	230		235		240	acc aat ttg aat gca ttg aaa gag ctt ata aca gag aat aaa acc gta	768	Thr Asn Leu Asn Ala leu Lys Glu Leu Ile Thr Glu Asn Lys Thr Val		245	250		255	ata gag caa cta aaa gct gat gct caa ctt aga gaa gag caa gtg cgg	816																																																																		
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Ile Asn Gln Leu Gln Leu His Thr Arg Leu Ser Asp Phe Gly Asp																																																																																																																											
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Ile Glu Gln Leu Lys Ala Asp Ala Gln Leu Arg Glu Glu Gln Val Arg 260 265 270	
ttt tta gaa aag cgt aaa caa gag tta gaa gag gct tgt tca aca ttg Phe Leu Glu Lys Arg Lys Gln Glu Leu Glu Glu Ala Cys Ser Thr Leu 275 280 285	864
tcc cat tca att gcg act cta cag gaa tcc aca acc ctt cta aag gac Ser His Ser Ile Ala Thr Leu Gln Glu Ser Thr Thr Leu Leu Lys Asp 290 295 300	912
tct aca act aac tta cat gca gtt gaa agt cgt ctt atc ggt gtt atg Ser Thr Thr Asn Leu His Ala Val Glu Ser Arg Leu Ile Gly Val Met 305 310 315 320	960
gtt cag gat ggt gca gag tcc tcc acc qta gag gaa gct tca caa gat Val Gln Asp Gly Ala Glu Ser Ser Thr Val Glu Glu Ala Ser Gln Asp 325 330 335	1008
gat agc gcg caa ccc caa gat gaa aat caa tct gat gct gga gag cat Asp Ser Ala Gln Pro Gln Asp Glu Asn Gln Ser Asp Ala Gly Glu His 340 345 350	1056
aaa gat agt taa Lys Asp Ser 355	1068
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Ile Pro Ile Ser Ile Glu Ala Pro Thr Ser Ser Ala Ala Ala Val Gly 35 40 45	
Ala Lys Thr Ala Ile Glu Pro Glu Gly Arg Ser Pro Leu Leu Gln Arg 50 55 60	
Ile Cys Tyr Leu Val Lys Ile Ile Ala Ala Ile Ala Leu Phe Val Val 65 70 75 80	
Gly Ile Ala Ala Leu Val Cys Leu Tyr Leu Gly Ser Val Ile Ser Thr 85 90 95	
Pro Ser Leu Ile Leu Met Leu Ala Ile Met Leu Val Ser Phe Val Ile 100 105 110	
Val Ile Thr Ala Ile Arg Asp Gly Thr Pro Ser Gln Val Val Arg His 115 120 125	
Met Lys Gln Gln Ile Gln Gln Phe Gly Glu Glu Asn Thr Arg Leu His 130 135 140	

WO 99/53948

PCT/US99/08744

Thr Ala Val Glu Asn Leu Lys Ala Val Asn Val Glu Leu Ser Glu Gln
145 150 155 160

Ile Asn Gln Leu Lys Gln Leu His Thr Arg Leu Ser Asp Phe Gly Asp
165 170 175

Arg Leu Glu Ala Asn Thr Gly Asp Phe Thr Ala Leu Ile Ala Asp Phe
180 185 190

Gln Leu Ser Leu Glu Glu Phe Lys Ser Val Gly Thr Lys Val Glu Thr
195 200 205

Met Leu Ser Pro Phe Glu Lys Leu Ala Gln Ser Leu Lys Glu Thr Phe
210 215 220

Ser Gln Glu Ala Val Gln Ala Met Met Ser Ser Val Thr Glu Leu Arg
225 230 235 240

Thr Asn Leu Asn Ala Leu Lys Glu Leu Ile Thr Glu Asn Lys Thr Val
245 250 255

Ile Glu Gln Leu Lys Ala Asp Ala Gln Leu Arg Glu Glu Gln Val Arg
260 265 270

Phe Leu Glu Lys Arg Lys Gln Glu Leu Glu Glu Ala Cys Ser Thr Leu
275 280 285

Ser His Ser Ile Ala Thr Leu Gln Glu Ser Thr Thr Leu Leu Lys Asp
290 295 300

Ser Thr Thr Asn Leu His Ala Val Glu Ser Arg Leu Ile Gly Val Met
305 310 315 320

Val Gln Asp Gly Ala Glu Ser Ser Thr Val Glu Glu Ala Ser Gln Asp
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Lys Asp Ser
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gac gtt tta ata gct ttt aat aga aag cta aat ctc gta gaa caa caa 96
Asp Val Leu Ile Ala Phe Asn Arg Lys Leu Asn Leu Val Glu Gln Gln
20 25 30

gcg aaa gaa ctt gaa acg aaa gtc agt ttg gta gac aga aca gct act	144
Lys Glu Leu Glu Thr Lys Val Ser Leu Val Asp Arg Thr Ala Thr	
35 40 45	
tta tca ctt acc act ggc aat aat gta gcc acg gat gta ctc ctt tta	192
Leu Ser Leu Thr Thr Gly Asn Asn Val Ala Thr Asp Val Leu Leu Leu	
50 55 60	
aaa gat gag gtt gca gaa cta aaa gga tgt ttg tct gca gtt acg gat	240
Lys Asp Glu Val Ala Glu Leu Lys Gly Cys Leu Ser Ala Val Thr Asp	
65 70 75 80	
cta tta atc cgc tca ggc tca tca aga aca cct ggg ggt gct cct aat	288
Leu Leu Ile Arg Ser Gly Ser Ser Arg Thr Pro Gly Gly Ala Pro Asn	
85 90 95	
cca gaa ggc act aat tac cta ata gga tgc aca cct cct tct ctt tgc	336
Pro Glu Gly Thr Asn Tyr Leu Ile Gly Cys Thr Pro Pro Ser Leu Cys	
100 105 110	
gct aaa ctt aca gcg tta gcg tta aca att ata gcc ctc att gct atc	384
Ala Lys Leu Thr Ala Leu Ala Leu Thr Ile Ile Ala Leu Ile Ala Ile	
115 120 125	
aca gta ctt gtt atc tgt att gtt act gtt tgc ggc ggt ttc ccc cta	432
Thr Val Leu Val Ile Cys Ile Val Thr Val Cys Gly Gly Phe Pro Leu	
130 135 140	
ttt att tcc cta ctc aac atg tac aca gtt ggt gct tgt atc tcc tta	480
Phe Ile Ser Leu Leu Asn Met Tyr Thr Val Gly Ala Cys Ile Ser Leu	
145 150 155 160	
ccg atc att tcg tgt gcc gca gtt tca atg atg att cta tgc tca cat	528
Pro Ile Ile Ser Cys Ala Ala Val Ser Met Met Ile Leu Cys Ser His	
165 170 175	
tct att aac tct tta tta aga aac agg cct gcg atc tat atg act aac	576
Ser Ile Asn Ser Leu Leu Arg Asn Arg Pro Ala Ile Tyr Met Thr Asn	
180 185 190	
aat ttt caa aca gaa tct taa	597
Asn Phe Gln Thr Glu Ser	
195	
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Ala Lys Glu Leu Glu Thr Lys Val Ser Leu Val Asp Arg Thr Ala Thr	
35 40 45	
Leu Ser Leu Thr Thr Gly Asn Asn Val Ala Thr Asp Val Leu Leu Leu	

50	55	60
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Lys Asp Glu Val Ala Glu Leu Lys Gly Cys Leu Ser Ala Val Thr Asp	70	75
65		80

Leu Leu Ile Arg Ser Gly Ser Ser Arg Thr Pro Gly Gly Ala Pro Asn	85	90
		95

Pro Glu Gly Thr Asn Tyr Leu Ile Gly Cys Thr Pro Pro Ser Leu Cys	100	105
		110

Ala Lys Leu Thr Ala Leu Ala Leu Thr Ile Ile Ala Leu Ile Ala Ile	115	120
		125

Thr Val Leu Val Ile Cys Ile Val Thr Val Cys Gly Gly Phe Pro Leu	130	135
		140

Phe Ile Ser Leu Leu Asn Met Tyr Thr Val Gly Ala Cys Ile Ser Leu	145	150
		155
		160

Pro Ile Ile Ser Cys Ala Ala Val Ser Met Met Ile Leu Cys Ser His	165	170
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Ser Ile Asn Ser Leu Leu Arg Asn Arg Pro Ala Ile Tyr Met Thr Asn	180	185
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Asn Phe Gln Thr Glu Ser	195
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	10
	15

tct tct tta tta aat ccg agt gat ctc aca aca cta tcc aac ctc	96
Ser Ser Leu Leu Asn Pro Ser Asp Leu Thr Thr Gln Leu Ser Asn Leu	
20	25
	30

cag act gtt ctc gca ggg ata caa caa caa cat cct tta aac ggt ggt	144
Gln Thr Val Leu Ala Gly Ile Gln Gln His Pro Leu Asn Gly Gly	
35	40
	45

tgg cct cag cat cat cct act ggc gct gca gat caa aat tat ctc atg	192
Trp Pro Gln His His Pro Thr Gly Ala Ala Asp Gln Asn Tyr Leu Met	
50	55
	60

cgt ctg cat atg caa tct cat atg gca agt acc gta tca gca gta tct gaa	240
Arg Leu Met Gln Ser His Met Ala Ser Thr Val Ser Ala Val Ser Glu	
65	70
	75
	80

tta aga acc gaa gtc act gca atc aag aca aaa ttg cac ggg cta tct	288
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Leu Arg Thr Glu Val Thr Ala Ile Lys Thr Lys Leu His Gly Leu Ser
 85 90 95
 act cca gct aat gtt tgc agc ggt cct atg gct cta gcc gct ttt ctt 336
 Thr Pro Ala Asn Val Cys Ser Gly Pro Met Ala Leu Ala Phe Leu
 100 105 110
 cta gct ata tct tta gtt gcg att atc atc att gtt tta gcc tcc tta 384
 Leu Ala Ile Ser Leu Val Ala Ile Ile Ile Val Leu Ala Ser Leu
 115 120 125
 ggc ctt gca ggc ata cta cct caa gct gcc gct atc tta gtg aat aca 432
 Gly Leu Ala Gly Ile Leu Pro Gln Ala Ala Ile Leu Val Asn Thr
 130 135 140
 gca aac tct ata tgg gct att gtt agc gct tcg ata gtc act gtt atc 480
 Ala Asn Ser Ile Trp Ala Ile Val Ser Ala Ser Ile Val Thr Val Ile
 145 150 155 160
 tgc tta att agc gtg cta tgc ata acg cta att cga cac cat aaa ccc 528
 Cys Leu Ile Ser Val Leu Cys Ile Thr Leu Ile Arg His His Lys Pro
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 35 40 45
 Trp Pro Gln His His Pro Thr Gly Ala Ala Asp Gln Asn Tyr Leu Met
 50 55 60
 Arg Leu Met Gln Ser His Met Ala Ser Thr Val Ser Ala Val Ser Glu
 65 70 75 80
 Leu Arg Thr Glu Val Thr Ala Ile Lys Thr Lys Leu His Gly Leu Ser
 85 90 95
 Thr Pro Ala Asn Val Cys Ser Gly Pro Met Ala Leu Ala Phe Leu
 100 105 110
 Leu Ala Ile Ser Leu Val Ala Ile Ile Ile Val Leu Ala Ser Leu
 115 120 125
 Gly Leu Ala Gly Ile Leu Pro Gln Ala Ala Ile Leu Val Asn Thr
 130 135 140

Ala Asn Ser Ile Trp Ala Ile Val Ser Ala Ser Ile Val Thr Val Ile
145 150 155 160

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165 170 175

Leu Pro Ile Glu Thr Arg Pro Thr Gly His
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<211> 822

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<221> CDS

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1 5 10 15	

tcc tac tca gcc aat cgc gta cct caa cct tct ttg atg gac aaa att	96
Ser Tyr Ser Ala Asn Arg Val Pro Gln Pro Ser Leu Met Asp Lys Ile	
20 25 30	

aag aaa ata gca gcc att gcc tcc cta att ctt ata ggc aca ata ggc	144
Lys Lys Ile Ala Ala Ile Ala Ser Leu Ile Leu Ile Gly Thr Ile Gly	
35 40 45	

ttt tta gct ctt ttg gga cat ctt gtt ggc ttt ctg atc gct cca caa	192
Phe Leu Ala Leu Leu Gly His Leu Val Gly Phe Leu Ile Ala Pro Gln	
50 55 60	

atc act att gtt ctt ctt gcc cta ttc att acc tca tta gca ggg aat	240
Ile Thr Ile Val Leu Ala Leu Ala Phe Ile Thr Ser Leu Ala Gly Asn	
65 70 75 80	

gct ctt tat cta cag aaa acc gct aat cta cat cta tac cag gat ctg	288
Ala Leu Tyr Leu Gln Lys Thr Ala Asn Leu His Leu Tyr Gln Asp Leu	
85 90 95	

caa aga gaa gtt ggg tct cta aaa gaa att aat ttc atg ctg agc gtt	336
Gln Arg Glu Val Gly Ser Leu Lys Glu Ile Asn Phe Met Leu Ser Val	
100 105 110	

cta cag aaa gaa ttt ctt cat tta tct aaa gaa ttt gca acg aca tct	384
Leu Gln Lys Glu Phe Leu His Leu Ser Lys Glu Phe Ala Thr Thr Ser	
115 120 125	

aaa gac ctc tot gct gta tct caa gat tat ttc tct tgt ttg caa gga	432
Lys Asp Leu Ser Ala Val Ser Gln Asp Phe Tyr Ser Cys Leu Gln Gly	
130 135 140	

ttt aga gat aac tat aaa ggt ttt gaa tct ctt ttg gat gag tat aaa	480
Phe Arg Asp Asn Tyr Lys Glu Phe Glu Ser Leu Asp Glu Tyr Lys	
145 150 155 160	

aac tct aca gaa gaa atg cgc aaa ctc ttt tcg caa gaa atc ata gca 528

Asn Ser Thr Glu Glu Met Arg Lys Leu Phe Ser Gln Glu Ile Ile Ala		
165	170	175

gat ctt aaa ggc tct gtt gcc tca tta aga gag gaa atc cga ttc cta	576	
Asp Leu Lys Gly Ser Val Ala Ser Leu Arg Glu Glu Ile Arg Phe Leu		
180	185	190

acc cca tta gca gaa gaa gtt cgc cga tta gcg cat aac cag gaa tca	624	
Thr Pro Leu Ala Glu Glu Val Arg Arg Leu Ala His Asn Gln Glu Ser		
195	200	205

tta aca gcg gct att gaa gaa tta aaa aca att cgt gat agc tta cga	672	
Leu Thr Ala Ala Ile Glu Glu Leu Lys Thr Ile Arg Asp Ser Leu Arg		
210	215	220

gat gaa att gga caa ctt tca caa ctt tct aaa act ctt acc agt caa	720		
Asp Glu Ile Gly Gln Leu Ser Gln Leu Ser Lys Thr Leu Thr Ser Gln			
225	230	235	240

att gca tta caa cga aaa gag agc tca gat ctg tgt tcc cag ata aga	768	
Ile Ala Leu Gln Arg Lys Glu Ser Ser Asp Leu Cys Ser Gln Ile Arg		
245	250	255

gag acg ctc tcc tcc ccc aga aag tct gca tca ccc tct aca aaa agc	816	
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Lys Lys Ile Ala Ala Ile Ala Ser Leu Ile Leu Ile Gly Thr Ile Gly		
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Phe Leu Ala Leu Leu Gly His Leu Val Gly Phe Leu Ile Ala Pro Gln		
50	55	60

Ile Thr Ile Val Leu Leu Ala Leu Phe Ile Thr Ser Leu Ala Gly Asn			
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Ala Leu Tyr Leu Gln Lys Thr Ala Asn Leu His Leu Tyr Gln Asp Leu		
85	90	95

Gln Arg Glu Val Gly Ser Leu Lys Glu Ile Asn Phe Met Leu Ser Val		
100	105	110

Leu Gln Lys Glu Phe Leu His Leu Ser Lys Glu Phe Ala Thr Thr Ser		
115	120	125

Lys Asp Leu Ser Ala Val Ser Gln Asp Phe Tyr Ser Cys Leu Gln Gly
 130 135 140

Phe Arg Asp Asn Tyr Lys Gly Phe Glu Ser Leu Leu Asp Glu Tyr Lys
 145 150 155 160

Asn Ser Thr Glu Glu Met Arg Lys Leu Phe Ser Gln Glu Ile Ile Ala
 165 170 175

Asp Leu Lys Gly Ser Val Ala Ser Leu Arg Glu Glu Ile Arg Phe Leu
 180 185 190

Thr Pro Leu Ala Glu Glu Val Arg Arg Leu Ala His Asn Gln Glu Ser
 195 200 205

Leu Thr Ala Ala Ile Glu Glu Leu Lys Thr Ile Arg Asp Ser Leu Arg
 210 215 220

Asp Glu Ile Gly Gln Leu Ser Gln Leu Ser Lys Thr Leu Thr Ser Gln
 225 230 235 240

Ile Ala Leu Gln Arg Lys Glu Ser Ser Asp Leu Cys Ser Gln Ile Arg
 245 250 255

Glu Thr Leu Ser Ser Pro Arg Lys Ser Ala Ser Pro Ser Thr Lys Ser
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gtc tct att caa ccc agt cag att cca acc agc aaa aaa gta atg att 96
 Val Ser Ile Gln Pro Ser Gln Ile Pro Thr Ser Lys Lys Val Met Ile
 20 25 30

gcg ata atg act ctt ttt gca ctc aca gcc att gca gca ata gtc ctt 144
 Ala Ile Met Thr Leu Phe Ala Leu Thr Ala Ile Ala Ile Val Leu
 35 40 45

tcc atc gtt aca gtt tgt gga ggg ttt cct ttt ctt ctt got gca ctt 192
 Ser Ile Val Thr Val Cys Gly Gly Phe Pro Phe Leu Leu Ala Ala Leu
 50 55 60

aac acc gta act att ggt gca tgc gta tcc ttg ccg gta ttc act tgc 240
 Asn Thr Val Thr Ile Gly Ala Cys Val Ser Leu Pro Val Phe Thr Cys
 65 70 75 80

ata gct aca acg tta tta ctt ctt tgt ctc cgt aat atc gaa ctc cta 288

Ile Ala Thr Thr Leu Leu Leu Cys Leu Arg Asn Ile Glu Leu Leu
85 90 95

gcc aga ccg caa gta ttt acc ctc tcc act caa ttc agc cca aca aaa 336
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100 105 110

cct caa gaa tag 348
Pro Gln Glu
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20 25 30

Ala Ile Met Thr Leu Phe Ala Leu Thr Ala Ile Ala Ala Ile Val Leu
35 40 45

Ser Ile Val Thr Val Cys Gly Gly Phe Pro Phe Leu Leu Ala Ala Leu
50 55 60

Asn Thr Val Thr Ile Gly Ala Cys Val Ser Leu Pro Val Phe Thr Cys
65 70 75 80

Ile Ala Thr Thr Leu Leu Leu Cys Leu Arg Asn Ile Glu Leu Leu
85 90 95

Ala Arg Pro Gln Val Phe Thr Leu Ser Thr Gln Phe Ser Pro Thr Lys
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Pro Gln Glu
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ccc acg tct ccc gct cca tca aga aaa cga gga tcc ttt ccc cca caa 96
Pro Thr Ser Pro Ala Pro Ser Arg Lys Arg Gly Ser Phe Pro Pro Gln
20 25 30

tct cct tct ggc gtc ttc tta gag gga gct aat ttc tct aca tgg 144
 Ser Pro Ser Ala Val Gly Ser Leu Glu Gly Ala Asn Phe Ser Thr Trp
 35 40 45

ggg cca ggc ccc ttc ttc act gtc cct gtt tat cca caa caa ctc gct 192
 Gly Pro Gly Pro Phe Phe Thr Val Pro Val Tyr Pro Gln Gln Leu Ala
 50 55 60

gca atg caa aac aac ctt ttt aca ttg caa aca gag gtt tct gct ctc 240
 Ala Met Gln Asn Asn Leu Phe Thr Leu Gln Thr Glu Val Ser Ala Leu
 65 70 75 80

aag aaa aaa tta gtt cag tct agt cag aca cgc gga tct tta gga ctc 288
 Lys Lys Lys Leu Val Gln Ser Ser Gln Thr Arg Gly Ser Leu Gly Leu
 85 90 95

ggc ccg cag ttt tta gcg gca tgc tta gtt gct gcg aca att ctt gca 336
 Gly Pro Gln Phe Leu Ala Ala Cys Leu Val Ala Ala Thr Ile Leu Ala
 100 105 110

gta gct gtt atc gta ctt gct tcc tta gga ctt ggc ggt gtt ctt cct 384
 Val Ala Val Ile Val Leu Ala Ser Leu Gly Leu Gly Val Leu Pro
 115 120 125

ttt gtc ctt gtt tgt ctg gct ggg tca act aat gca att tgg gct att 432
 Phe Val Leu Val Cys Leu Ala Gly Ser Thr Asn Ala Ile Trp Ala Ile
 130 135 140

gtg agc gcc tcc atc act aca ctg att tgt tgc gtt tcc atc gct tgc 480
 Val Ser Ala Ser Ile Thr Leu Ile Cys Cys Val Ser Ile Ala Cys
 145 150 155 160

atc ttc tta gca aaa tgt gat aag gga tct gat cct caa act tta tat 528
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 165 170 175

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 Val Ser

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Ser Pro Ser Ala Val Gly Ser Leu Glu Gly Ala Asn Phe Ser Thr Trp
 35 40 45

Gly Pro Gly Pro Phe Phe Thr Val Pro Val Tyr Pro Gln Gln Leu Ala
 50 55 60

Ala Met Gln Asn Asn Leu Phe Thr Leu Gln Thr Glu Val Ser Ala Leu
 65 70 75 80

Lys Lys Lys Leu Val Gln Ser Ser Gln Thr Arg Gly Ser Leu Gly Leu
85 90 95

Gly Pro Gln Phe Leu Ala Ala Cys Leu Val Ala Ala Thr Ile Leu Ala
100 105 110

Val Ala Val Ile Val Leu Ala Ser Leu Gly Leu Gly Gly Val Leu Pro
115 120 125

Phe Val Leu Val Cys Leu Ala Gly Ser Thr Asn Ala Ile Trp Ala Ile
130 135 140

Val Ser Ala Ser Ile Thr Thr Leu Ile Cys Cys Val Ser Ile Ala Cys
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D-1a 01/18/2001
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100L 1 54 3a

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VERIFICATION SUMMARY
PATENT APPLICATION US/09/673,763 D-22 JI/13/2001

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G:10 R:270 C: Current Application Number differs, Replaced Application Number
G:11 R:271 C: Current Filing Date differs, Replaced Current Filing Date

**COMBINED DECLARATION AND POWER OF ATTORNEY
FOR PATENT APPLICATION**

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I believe I am an original, first and joint inventor of the subject matter which is claimed and for which a patent is sought on the invention entitled CHLAMYDIA PROTEINS AND THEIR USES, the specification of which

- is attached hereto.
- was filed on _____ as Application No. _____.
- was described and claimed in PCT International Application No. _____, filed on _____.
- and was amended on _____ (if applicable).
- with amendments through _____ (if applicable).

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to patentability as defined in Title 37, Code of Federal Regulations, Section 1.56. If this is a continuation-in-part application filed under the conditions specified in 35 U.S.C. § 120 which discloses and claims subject matter in addition to that disclosed in the prior copending application, I further acknowledge the duty to disclose material information as defined in 37 C.F.R. § 1.56 which occurred between the filing date of the prior application and the national or PCT international filing date of the continuation-in-part application.

I hereby claim foreign priority benefits under Title 35, United States Code, Section 119(a)-(d) of any foreign application(s) for patent or inventor's certificate or of any PCT International application(s) designating at least one country other than the United States of America listed below and have also identified below any foreign application(s) for patent or inventor's certificate or any PCT International application(s) designating at least one country other than the United States of America filed by me on the same subject matter having a filing date before that of the application(s) on which priority is claimed:

Prior Foreign Application(s)	Priority Claimed			
(Number)	(Country)	(Day/Month/Year Filed)	Yes	No

I hereby claim the benefit under Title 35, United States Code, Section 119(e) of any United States provisional application(s) listed below:

60/082,438	20 April 1998
60/082,588	21 April 1998
60/086,450	22 May 1998
Application Number	Filing Date

I hereby claim the benefit under Title 35, United States Code, Section 120 of any United States application(s) or Section 365(c) of any PCT International application(s) designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of Title 35, United States Code, Section 112, I acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, Section 1.56(a) which occurred between the filing date of the prior application and the national or PCT International filing date of this application:

PCT/US99/08744 (Application No.)	20 April 1999 (Filing Date)	Published (Status)
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The undersigned hereby authorizes the U.S. attorney or agent named herein to accept and follow instructions from _____ as to any action to be taken in the Patent and Trademark Office regarding this application without direct communication between the U.S. attorney or agent and the undersigned. In the event of a change in the persons from whom instructions may be taken, the U.S. attorney or agent named herein will be so notified by the undersigned.

I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application, to file a corresponding international application, and to transact all business in the Patent and Trademark Office connected therewith:

Customer Number

-OR-

Registered practitioners listed below:



24197

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KLITZKE II, Ramon A.	30,188	VAN DENBERG, John D.	31,312
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MAURER, Gregory L.	43,781	WIGHT, Stephen A.	37,759
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Address all telephone calls to Tanya M. Harding, Ph.D. at telephone number (503) 226-7391.

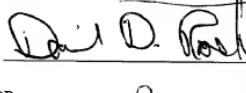
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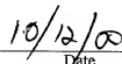
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LEIGH & WHINSTON, LLP
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I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Full Name of Sole or first Inventor:

Daniel D. Rockey


Inventor's Signature


Date

Residence: Corvallis, OR

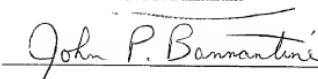

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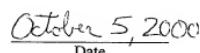
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Full Name of Second Inventor:

John P. Bannantine


Inventor's Signature


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